

BD

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
1 July 2004 (01.07.2004)

PCT

(10) International Publication Number  
**WO 2004/055519 A2**

(51) International Patent Classification<sup>7</sup>: **G01N 33/68,**  
33/574

Peking Union Medical Coll, ege Hospital, Chinese Acad-  
emy of Science, Peking U, nion Medical College, Beijing  
100730, P.R. (CN). **SHEN, Yan**; c/o Chinese National  
Human Genome Center,, Beijing SinoGenoMax Co. Ltd.,  
#3-707 North Yongchang Road BDA, Beijing 100176  
(CN).

(21) International Application Number:  
PCT/EP2003/014057

(22) International Filing Date:  
11 December 2003 (11.12.2003)

(74) Common Representative: **WITTE, Hubert**; 124 Gren-  
zacherstrasse, CH-4070 Basel (CH).

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
02028058.2 17 December 2002 (17.12.2002) EP  
03025237.3 5 November 2003 (05.11.2003) EP

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,  
CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE,  
GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR,  
KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK,  
MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT,  
RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR,  
TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW.

(71) Applicants: **F. HOFFMANN-LA ROCHE AG**  
[CH/CH]; 124 Grenzacherstrasse, CH-4070 Basel (CH).  
**SINOGENOMAX CO. LTD. CHINESE NATIONAL**  
**HUMAN GENOMECENTER** [CN/CN]; 3#-707 North  
Yongchang Road BDA, 100176 Beijing, PR. (CN).

(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),  
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,  
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,  
SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,  
GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors: **CHEN, Jie**; Department of Pathology, Peking  
Union Medical Coll, ege Hospital, Chinese Academy of  
Medical Science,, Peking Union Medical College, Beijing  
100730 P.R. (CN). **HU, Liping**; National Laboratory of  
Medical Molecular Biology,, Institute of Basic Medical  
Sciences, Chinese Aca, demy of Medical Science + Peking  
Union Medical Col, lege, Beijing 100005, P.R. (CN).  
**LIU, Tong, Hua**; Department of Pathology, Peking Union  
Medical Coll, ege Hospital, Chinese Academy of Medical  
Science,, Peking Union Medical College, Beijing 100730,  
P.R. (CN). **LU, Zhao, Hui**; Department of Pathology,

#### Published:

— without international search report and to be republished  
upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

(54) Title: SPECIFIC MARKERS FOR PANCREATIC CANCER

(57) Abstract: The present invention provides polypeptides which are up- or down-regulated in pancreatic cancer and which can be used as markers for diagnosis of pancreatic cancer. The invention also provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of one or more polypeptides as disclosed herein. Furthermore, screening methods relating to inhibitors and antagonists of the specific polypeptides disclosed herein are provided.

WO 2004/055519 A2

### Specific Markers for Pancreatic Cancer

The present invention relates to markers for diagnosis of pancreatic cancer comprising at least one polypeptide identified by proteomics to be up-regulated in pancreatic cancer, to an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of specific markers as disclosed  
5 herein. Furthermore, screening methods relating to antagonists of the specific markers disclosed herein are provided.

10 Pancreatic cancer is a common cause of death in the Western world. It is one of the most aggressive malignant tumors, with an overall 5-year survival rate of 0.4%. In many patients with pancreatic cancer, accurate preoperative diagnosis is difficult to achieve with conventional imaging analyses. Most patients with pancreatic cancer present late in the course of the disease and have either locally extensive or metastatic disease. Overall,  
15 only up to 20% are candidates for resection and have the potential for curative surgery. Among the causes for this late presentation is the lack of diagnostic methods for an earlier detection of the disease. Besides this lack of diagnostic methods, the high mortality of patients with pancreatic cancer is additionally caused by a lack of effective treatments. Therefore, the identification of new targets for early diagnosis of pancreatic tumors, and  
20 for the development of agents to treat pancreatic cancer is a challenge of paramount importance.

The problem of identifying polypeptides suitable as markers of pancreatic cancer  
25 for early diagnosis of the disease, and the long felt need for such markers, was overcome by the present invention by applying the new technology of proteomics. It was surprisingly found by using proteomic technology that a specific set of polypeptides are differentially expressed in pancreatic tissue obtained from individuals suffering from  
HR/03.11.2003

pancreatic cancer, as compared to healthy pancreatic tissue. Said differentially expressed polypeptides are listed in appended tables 2 and 3. The polypeptides in table 3 are encoded by genes which were previously identified to be up-regulated in pancreatic cancer on the transcriptional level (Iacobuzio-Donahue et al., (2002), Am. J. Pathol. 160, 1239-1249). However, it is well known that regulation on the transcriptional level is not necessarily indicative of a similar regulation of the expression of the respective gene on the translational level. Thus, only by demonstrating that the polypeptides listed in table 3 are up-regulated in pancreatic cancer is it possible to use them for polypeptide-based diagnostic assays for the detection of pancreatic cancer.

10

Based on the polypeptides listed in tables 2 and 3, the present invention provides a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3 (Seq ID No. 1 to 24 and 26 to 49; and/or Seq ID No. 25 and 50 to 55). Thus, the term "marker" as used herein refers to one or more polypeptides that are regulated in cancer and that can be used to diagnose pancreatic cancer or a susceptibility to pancreatic cancer either alone or as combinations of multiple polypeptides that are known to be regulated in pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48; and/or Seq ID No. 25 and 50 to 54. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40; and/or Seq ID No. 50 to 52. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 and/or Seq ID No. 51 and 52. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31; and/or Seq ID No. 52.

25

The term "polypeptide" as used herein, refers to a polymer of amino acids, and not to a specific length. Thus, peptides, oligopeptides and proteins are included within the definition of polypeptide.

30

Preferably, the marker of this invention is a marker comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 2.

Furthermore, a polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3, is used as a marker or as part of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48 from table 2 and/or Seq ID No. 25 and 50 to 54 from table 3. These polypeptides are induced at least two fold, as can be seen in tables 2 and 3. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40 from table 2 and/or Seq ID No. 50 to 52 from table 3. These polypeptides are induced at least three fold, as can be seen in tables 2 and 3. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 from table 2 and/or Seq ID No. 51 and 52 from table 3. These polypeptides are induced at least 4 fold, as can be seen in tables 2 and 3. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31 from table 2 and/or Seq ID No. 52 from table 3, which are the polypeptides that are induced five fold, as shown in tables 2 and 3.

The present invention pertains to a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6. Preferably, said at least one polypeptide additionally does not include Seq ID No.s 25 and 50 to 55.

In a preferred embodiment, the marker hereinbefore described additionally comprises at least one of the polypeptides listed in table 5.

Several groups of polypeptides were identified as markers for pancreatic cancers:

#### Enzymes

One of the enzymes that caught our attention was Glutamine  $\gamma$ -glutamyltransferase/tissue transglutaminase (TGLC, Seq ID No. 54). It is a member of the transglutaminase family that catalyzes  $\text{Ca}^{2+}$  dependent reactions resulting in the post translational modification (cross-linking and conjugation with polyamines) of proteins at



the level of glutamine and lysine residues (Greenberg, C. S., Birckbichler, P. J., and Rice, R. H. Transglutaminases: multifunctional cross-linking enzymes that stabilize tissues. *FASEB J.*, 5: 3071-3077, 1991). Many different roles for this protein have been described, among them apoptosis, adhesion, and differentiation (Amendola, A., Fesus, L., Piacentini, M., and Szondy, Z. "Tissue" transglutaminase in AIDS. *J. Immunol. Methods*, 265: 145-159, 2002). There is some controversy on the role of TGLC in apoptosis. While several pieces of evidence suggest that TGLC is a pro-apoptotic protein (Melino, G., et al., *Mol. Cell Biol.*, 14: 6584-6596, 1994), Jason et al. found that TGLC acts in anti-apoptotic fashion (Boehm, J. E., et al. *J. Biol. Chem.*, 277: 20127-20130, 2002). Many substrates of TGLC are major extra-cellular matrix (ECM) components such as fibronectin, osteonectin, and collagen, which makes TGLC an important enzyme in ECM development (Raghunath, M., et al., *J. Clin. Invest.*, 98: 1174-1184, 1996., Nemes, Z., Jr., et al. *J. Biol. Chem.*, 272: 20577-20583, 1997). Abnormal ECM development is involved in many pathological conditions such as fibrosis and may play a role in the proliferation of fibrous tissue observed in PC. Haroon et al. described that TGLC ECM-promoting abilities are an important part of the host response mechanism against tumor growth (Haroon, Z. A., et al., *Lab Invest*, 79: 1679-1686, 1999). Interestingly, loss of TGLC can be a biomarker for prostate adenocarcinoma (Birckbichler, P. J., et al., *Cancer*, 89: 412-423, 2000), which raises the question whether the measured TGLC is produced by neoplastic ductal cells and/or stromal cells. Measurements of mRNA levels in PC, normal tissue and PC cell lines indicate that TGLC is over expressed in both cell types (Iacobuzio-Donahue, C. A., et al., *Am. J. Pathol.*, 160: 1239-1249, 2002), which would distinguish PC from prostate adenocarcinoma.. Therefore, one preferred embodiment of the present invention is a marker comprising Seq ID No. 54.

## 25 Cytoskeletal proteins

Several cytoskeletal proteins were detected at higher levels in PC than in surrounding tissue. One of these is gelsolin (Seq ID No. 3), a  $\text{Ca}^{2+}$  and PIP2 (polyphosphoinositide 4,5-bisphosphate) regulated severing and capping protein, which is a multifunctional actin regulatory protein and has roles in actin remodeling, motility, signaling, apoptosis and cancer (Maruta, H. G proteins cytoskeleton and cancer. Austin, Tex.: R.G. Landes, 1998). In several cancer studies, gelsolin expression has been described as down-regulated during carcinogenesis (breast, colon, stomach, bladder, prostate, and lung) (Asch, H. L., et al., *Cancer Res.*, 56: 4841-4845, 1996; Dosaka-Akita, H., et al., *Cancer Res.*, 58: 322-327, 1998, Prasad, S. C., et al. *Electrophoresis*, 18: 629-637, 1997). Another example for an up-regulated cytoskeletal protein is fascin (Seq ID No. 58), an

actin-bundling protein that has a role in cell matrix adhesion, cell interaction and migration. Fascin over expression has been reported in several cancers, such as breast, colon, and ovarian carcinoma (29). The present invention also features fascin 2 as a polypeptide up-regulated in pancreatic cancer (Seq ID No. 56). Thus, a preferred  
5 embodiment of the present invention is a marker comprising Seq ID. No. 3. In another preferred embodiment, the marker comprises Seq. ID No. 58. In another preferred embodiment, the marker comprises Seq. ID No. 56.

In our study, cytokeratin 7 (Seq. ID No. 52) and cytokeratin 19 (Seq ID No. 33) showed strong expression in PC. Both have also been described in other cancers and have  
10 been linked with metastasis formation (Moll, R., *Int.J.Biol.Markers*, 9: 63-69, 1994.). High protein levels of actinin-4 (Seq ID No. 5) were detected in PC. This protein was linked by others with cell motility and cancer invasion (Honda, K., Yamada, T., Endo, R., Ino, Y., Gotoh, M., Tsuda, H., Yamada, Y., Chiba, H., and Hirohashi, S. *J.Cell Biol.*, 140: 1383-1393, 1998.). Taken together, the apparent strong expression of cytoskeletal  
15 proteins is likely to be an important factor in the strong invasiveness and metastasis-forming potential of PC. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 52. In another preferred embodiment, the marker comprises Seq. ID No. 33. In another preferred embodiment, the marker comprises Seq. ID No. 5.

## 20 Metastasis

Cancer of exocrine pancreas is characterized by extensive local invasion, early lymphatic and hematogenous metastasis. Metastasis in PC has been found in the skeleton, eye, bladder, etc. The extent of angiogenesis depends on the balance between pro-angiogenic or anti-angiogenic factors released from cancer and host cell. Currently,  
25 intratumoral microvessel density (IMD) measured by immunocytochemistry appears to be the most reliable parameter for assessing angiogenic activity. Patients with high IMD have decreased survival rates in a variety of cancers (Fujioka, S., et al., *Cancer*, 92: 1788-1797, 2001). Thymidine phosphorylase (TYPH or TP, Seq ID No. 31) which is identical to platelet-derived endothelial cell growth factor, is strongly expressed in PC and  
30 stimulates the chemotaxis of endothelial cells through the 2-deoxy-D-ribose, degradation products of thymidine by TP, thus indirectly inducing angiogenesis (Haraguchi, M., et al. *Nature*, 368: 198, 1994.). Shuichi Fujioka et al. found that IMD and TP status were independent predictive indicators for overall as well as relapse-free survival in PC (Fujioka, S., et al., *Cancer*, 92: 1788-1797, 2001). An additional protein detected at higher  
35 levels in PC than in surrounding tissue likely involved in metastasis formation is

osteoblast specific factor 2 (Seq ID No.53), a putative bone adhesion protein. Breast carcinoma commonly metastasizes to bone (Guise, T. A. Cancer, 88: 2892-2898, 2000). Although the role of this protein in PC is not clearly established, our findings suggest a similar role for osteoblast specific factor 2 in PC. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 31. In another preferred embodiment, the marker comprises Seq. ID No. 53.

### Small GTP-binding proteins

Four small GTP-binding proteins and interacting proteins were more strongly expressed in PC than in normal pancreas tissue. These include RAN (Seq. ID No. 27), GBLP (guanine nucleotide binding protein  $\beta$  subunit-like protein RACK1, Seq. ID No. 47), GDIR (Rho GDP dissociation inhibitor 1, Seq. ID No. 55), and IQG1 or IQGAP1 (Ras gtpase activating like protein, Seq ID No. 25). Small GTP-binding proteins constitute a superfamily, which is structurally classified into at least five families: the Ras, Rho, Rab, Sar1/Arf, and Ran families and are involved in the regulation of gene expression, cytoskeletal reorganization, and nucleocytoplasmic transport (Takai, Y., et al. Physiol Rev., 81: 153-208, 2001). RAN is known to enhance androgen receptor-mediated transactivation and was shown to be overexpressed in prostate cancer (Sampson, E. R., et al., J.Biol.Regul.Homeost.Agents, 15: 123-129, 2001). Increased expression of RAN in 81% of prostate tumor cases, may contribute to over proliferation of prostate tumor cells (Li, P., et al., Am J Pathol., 161: 1467-1474, 2002). GBLP is an anchoring protein for activated protein kinase C $\beta$  and a variety of other proteins. Protein kinase C plays an important role in angiogenesis and cancer growth. Berns et al. found GBLP up-regulated in during angiogenesis *in vitro* and also associated with nonendothelial cells in angiogenically active tissue (Berns, H., et al., FASEB J., 14: 2549-2558, 2000). Further more, mRNA expression of GBLP is detected in epithelial cells of human colon carcinoma and proliferating epithelial cell of normal colon tissue. Therefore, there is a likely link between high GBLP expression and tumor growth. GDIR (Rho GDP dissociation inhibitor) had been found up-regulated in a chemoresistant fibrosarcoma cell line by 2D-PAGE (Sinha, P., et al., Electrophoresis, 20: 2961-2969, 1999) and may block apoptotic signal pathway mediated by Ras and c-jun kinase, resulting in the increase resistance against environmental stress. IQG1 (Ras GTPase-activating-like protein) is a widely expressed 190-kDa Cdc42-, Rac1-, and calmodulin-binding protein that interacts with F-actin *in vivo* and that can cross-link F-actin microfilaments *in vitro*. IQG1 negatively regulates the Ecc-based (E-cadherin/catenin complex) cell-cell adhesion by dissociating alpha-catenin. Up-regulation of IQGAP1 is correlated with the malignant

phenotype in gastric cancer (Sugimoto, N., et al., *J. Hum. Genet.*, 46: 21-25, 2001). By immunohistochemical analysis, IQGAP1 was found overexpressed in colorectal carcinoma and associated with carcinoma invasion (Nabeshima, K., et al., *Cancer Lett.*, 176: 101-109, 2002). Since cancer invasiveness is associated with the localized disruption of cell-cell adhesion, both our results and Iacobuzio-Donahue et al.'s data suggest that IQGAP1 may be involved in the disruption of local adhesion and in PC invasion to surrounding tissue. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 27. In another preferred embodiment, the marker comprises Seq. ID No. 47. In another preferred embodiment, the marker comprises Seq. ID No. 55. In another preferred embodiment, the marker comprises Seq. ID No. 25.

### S100 protein family

Another protein with high-level expression in PC is S109 (S100A9, MRP-14, calgranulin B, Seq ID No. 49), a member of the S100 protein family of highly homologous low molecular weight calcium binding proteins. Calgranulins are characterized by cell type-specific expression in cells of epithelial, myeloid and endothelial origin and accumulation at sites of acute and chronic inflammation (e.g. rheumatoid arthritis, cystic fibrosis, psoriasis, allergic dermatitis, inflammatory bowel diseases) (Donato, R. *Int.J.Biochem.Cell Biol.*, 33: 637-668, 2001). S100A8 and S100A9 can form a noncovalent heterodimer protein complex called calprotectin. Current reports support that both of S100A9 and S100 A8 have wide range of possible intracellular as well as extracellular functions (Schafer, B. W. and Heizmann, C. W. *Trends Biochem.Sci.*, 21: 134-140, 1996). S100A8 and S100A9 are negatively regulated by glucocorticoids in a c-Fos-dependent manner and over expressed throughout skin carcinogenesis (Gebhardt, C., et al., *Oncogene*, 21: 4266-4276, 2002). These proteins are also more strongly expressed in colorectal carcinoma than in matched normal colon mucosa, as shown by proteomics analysis (Stulik, J., et al., *Electrophoresis*, 20: 1047-1054, 1999). S100A9 has been detected in cultured human adenocarcinoma (AC) cells derived from various organs, and is associated with tumor differentiation in pulmonary adenocarcinoma (Arai, K., et al., *Oncol.Rep.*, 8: 591-596, 2001). Iacobuzio-Donahue et al.'s work indicates that over expression of S100A4 in PC is associated with poor differentiation and DNA hypomethylation (Rosty, C., et al., *Am.J.Pathol.*, 160: 45-50, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 49.

### Annexin

We found that annexin 1 (Seq ID No. 51) and annexin 2 (Seq ID No. 19) have high level of expression in PC. Both are members of a family of  $\text{Ca}^{2+}$ -dependent membrane-binding proteins. Described functions include, among others, an important role in malignant transformation (Masaki, T., et al., *Hepatology*, 24: 72-81, 1996), the control of epithelial cell line proliferation (Solito, E., et al., *Cell Growth Differ.*, 9: 327-336, 1998), and mediation of apoptosis (Canaider, S., et al., *Life Sci.*, 66: L265-L270, 2000). Evidence in support of causative roles for any annexins in the development of cancer is still mainly circumstantial. In MCF-7 breast carcinoma cells, overexpression of annexin1 led to abrogation of  $\text{Ca}^{2+}$  release after activation of purinergic or bradykinin receptors (Frey, B. M., et al., *FASEB J.*, 13: 2235-2245, 1999), while over expression of annexin1 in rat 2 fibroblasts leads to direct inhibition of cytosolic PLA<sub>2</sub>, which in turn depresses the serum response element of c-fos (Oh, J., et al., *FEBS Lett.*, 477: 244-248, 2000). Collectively, these studies imply a growth-suppressive role for annexin1. These results are not supported by the finding that annexin 1 is strongly up-regulated in a prostate cancer cell line (Vaarala, M. H., *Lab Invest*, 80: 1259-1268, 2000), esophageal cancer (Emmert-Buck, M. R., et al., *Mol.Carcinog.*, 27: 158-165, 2000), a stomach cancer cell line (Sinha, P., et al., *J.Biochem.Biophys.Methods*, 37: 105-116, 1998), mammary adenocarcinoma (Pencil, S. D. and Toth, M. *Clin.Exp.Metastasis*, 16: 113-121, 1998), and hepatocarcinoma (de Coupade, C., et al., *Hepatology*, 31: 371-380, 2000). In hepatocarcinoma, study also showed that the proliferative rate of both normal and malignant hepatocytes was attenuated by antisense to annexin 1. These and our data suggest that cell growth is associated with elevated rather than reduced levels of annexin 1, which is also supported by the studies of Iacobuzio- Donahue et al. (*Am. J. Pathol.*, 160: 1239-1249, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 51. In another preferred embodiment, the marker comprises Seq. ID No. 19.

Some additional proteins highly expressed in PC may have either clear roles in PC or an indirect link with PC, e.g. BGH3 (TGF- $\beta$ 1-induced protein, Seq ID No. 6) which is a secretory protein and acts as a marker for biologically active TGF-  $\beta$  1 (Langham, R. G., et al., *Transplantation*, 72: 1826-1829, 2001). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 6.

With the identification of polypeptides regulated in pancreatic cancer, the present invention provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of obtaining a biological sample; and detecting and/or measuring the increase of a marker described hereinbefore. The term "detection" as used herein refers to the qualitative determination of the absence or presence of polypeptides. The term "measured" as used herein refers to the quantitative determination of the differences in expression of polypeptides in biological samples from patients with pancreatic cancer and biological samples from healthy individuals. Methods for detection and/or measurement of polypeptides in biological samples are well known in the art and include, but are not limited to, Western-blotting, ELISAs or RIAs . Antibodies recognizing the polypeptides listed in table 2, 3, 5 and/or 6 can either be generated for the purpose of detecting said polypeptides, eg. by immunizing rabbits with purified proteins, or known antibodies recognizing said polypeptides can be used. For example, an antibody capable of binding to the denatured proteins, such as a polyclonal antibody, can be used to detect the peptides of this invention in a Western Blot. An example for a method to measure a marker is an ELISA. This type of protein quantitation is based on an antibody capable of capturing a specific antigen, and a second antibody capable of detecting the captured antigen. A further method for the detection of a diagnostic marker for pancreatic cancer is by analysing biopsy specimens for the presence or absence of the markers of this invention. Methods for the detection of these markers are well known in the art and include, but are not limited to, immunohistochemistry or immunofluorescent detection of the presence or absence of the polypeptides of the marker of this invention. Methods for preparation and use of antibodies, and the assays mentioned hereinbefore are described in Harlow, E. and Lane, D. Antibodies: A Laboratory Manual, (1988), Cold Spring Harbor Laboratory Press.

The accuracy of the diagnosis of pancreatic cancer can be increased by analysing combinations of multiple polypeptides listed in tables table 2, 3, 5 and/or 6. Thus, the in vitro method herein before described, comprises a marker which comprises at least two, preferably at least three, more preferably at least four, even more preferably at least five, and most preferably at least six of the polypeptides listed in table 2,3, 5 and/or 6.

For diagnosis of pancreatic cancer, suitable biological samples need to be analysed for the presence or absence of a marker. Said biological samples can be serum, plasma,

pancreatic juice or cells of pancreatic tissue. Cells from pancreatic tissue can be obtained by ERCP, secretin stimulation, fine-needle aspiration, cytologic brushings and large-bore needle biopsy.

- 5 It is also possible to diagnose pancreatic cancer by detecting and/or measuring nucleic acid molecules coding for the marker hereinbefore described. Preferably, said nucleic acid molecule is RNA or DNA. In another embodiment, said DNA is a cDNA.

- 10 In one embodiment of the present invention, the in vitro method herein before described comprises comparing the expression levels of at least two of the nucleic acids encoding said polypeptides in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer, to the expression levels of the same nucleic acids in a healthy individual.

- 15 In another embodiment of the present invention the in vitro method herein before described comprises comparing the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer to the expression levels of the same marker in a healthy individual. In a more preferred embodiment of the in vitro method, an increase or decrease of the expression levels of  
20 said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

- The present invention also provides a screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of contacting  
25 said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and detecting the interaction between said compound or plurality of compounds with said polypeptide.

- The "interaction" in the screening methods as disclosed herein may be measured by  
30 conventional methods. The type of conventional method for testing the interaction of a

compound with a polypeptide that is soluble, as opposed to membrane associated, can be an in vitro method using either purified recombinant polypeptide, or native polypeptide purified from cells that endogenously express the polypeptide. As a non-limiting example, a polypeptide of the invention can be bound to beads or immobilized on plastic or other surfaces, and interaction of a compound with the polypeptide can be measured by either using a labelled compound and measuring the label bound to the polypeptide or by displacement of a labeled known ligand from said polypeptide.

For polypeptides that are associated with the cell membrane on the cell surface, or which are expressed as transmembrane or integral membrane polypeptides, the interaction of a compound with said polypeptides can be detected with different methods which include, but are not limited to, methods using cells that either normally express the polypeptide or in which the polypeptide is overexpressed, eg. by detecting displacement of a known ligand which is labeled by the compound to be screened. Alternatively, membrane preparations may be used to test for interaction of a compound with such a polypeptide

Interaction assays to be employed in the method disclosed herein may comprise FRET-assays (fluorescence resonance energy transfer; as described, inter alia, in Ng, Science 283 (1999), 2085-2089 or Ubarretxena-Belandia, Biochem. 38 (1999), 7398-7405), TR-FRETs and biochemical assays as disclosed herein. Furthermore, commercial assays like "Amplified Luminescent Proximity Homogenous Assay<sup>TM</sup>" (BioSignal Packard) may be employed. Further methods are well known in the art and, inter alia, described in Fernandez, Curr. Opin. Chem. Biol. 2 (1998), 547-603.

25

The "test for interaction" may also be carried out by specific immunological and/or biochemical assays which are well known in the art and which comprise, e.g., homogenous and heterogenous assays as described herein below. Said interaction assays employing read-out systems are well known in the art and comprise, inter alia, two-hybrid screenings (as, described, inter alia, in EP-0 963 376, WO 98/25947, WO 00/02911; and as exemplified in the appended examples), GST-pull-down columns, co-precipitation assays from cell extracts as described, inter alia, in Kasus-Jacobi, Oncogene 19 (2000), 2052-2059, "interaction-trap" systems (as described, inter alia, in US



6,004,746) expression cloning (e.g. lamda gt11), phage display (as described, inter alia, in US 5,541,109), in vitro binding assays and the like. Further interaction assay methods and corresponding read out systems are, inter alia, described in US 5,525,490, WO 99/51741, WO 00/17221, WO 00/14271 or WO 00/05410. Vidal and Legrain (1999) in Nucleic  
5 Acids Research 27, 919-929 describe, review and summarize further interaction assays known in the art which may be employed in accordance with the present invention.

Homogeneous (interaction) assays comprise assays wherein the binding partners remain in solution and comprise assays, like agglutination assays.  
10 Heterogeneous assays comprise assays like, inter alia, immuno assays, for example, Enzyme Linked Immunosorbent Assays (ELISA), Radioactive Immunoassays (RIA), Immuno Radiometric Assays (IRMA), Flow Injection Analysis (FIA), Flow Activated Cell Sorting (FACS), Chemiluminescent Immuno Assays (CLIA) or Electrogenenerated Chemiluminescent (ECL) reporting.

15

The present invention further provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting said polypeptide with a compound identified and/or obtained by  
20 the screening method described above under conditions which allow interaction of said compound with said polypeptide; b) determining the activity of said polypeptide; c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison  
25 to (c) is indicative for an inhibitor or antagonist. The terms inhibitors and antagonists as used herein are used interchangeably. This screening assay can be performed either as an in vitro assay, or as a host-based assay. The host to be employed in the screening methods of the present invention and comprising and/or expressing a polypeptide listed in table 2, 3, 5 and/or 6 may comprise prokaryotic as well as eukaryotic cells. Said cells may  
30 comprise bacterial cells, yeast cells, as well as cultured (tissue) cell lines, inter alia, derived from mammals. Furthermore animals may also be employed as hosts, for example an non-human transgenic animal. Accordingly, said host (cell) may be transfected or transformed with the vector comprising a nucleic acid molecule coding for a polypeptide which is differentially regulated in pancreatic cancer as disclosed herein. Said host cell or  
35 host may therefore be genetically modified with a nucleic acid molecule encoding such a

polypeptide or with a vector comprising such a nucleic acid molecule. The term "genetically modified" means that the host cell or host comprises in addition to its natural genome a nucleic acid molecule or vector coding for a polypeptide listed in table 2, 3, 5 and/or 6 or at least a fragment thereof. Said additional genetic material may be introduced  
5 into the host (cell) or into one of its predecessors/parents. The nucleic acid molecule or vector may be present in the genetically modified host cell or host either as an independent molecule outside the genome, preferably as a molecule which is capable of replication, or it may be stably integrated into the genome of the host cell or host.

10 As mentioned herein above, the host cell of the present invention may be any prokaryotic or eukaryotic cell. Suitable prokaryotic cells are those generally used for cloning like *E. coli* or *Bacillus subtilis*. Yet, these prokaryotic host cells are also envisaged in the screening methods disclosed herein. Furthermore, eukaryotic cells comprise, for example, fungal or animal cells. Examples for suitable fungal cells are yeast cells,  
15 preferably those of the genus *Saccharomyces* and most preferably those of the species *Saccharomyces cerevisiae*. Suitable animal cells are, for instance, insect cells, vertebrate cells, preferably mammalian cells, such as e.g. CHO, HeLa, NIH3T3 or MOLT-4. Further suitable cell lines known in the art are obtainable from cell line depositories, like the American Type Culture Collection (ATCC).

20 The hosts may also be selected from non-human mammals, most preferably mice, rats, sheep, calves, dogs, monkeys or apes. As described herein above, said animals/mammals also comprise non-human transgenic animals, which preferably express at least one polypeptide differentially regulated in pancreatic cancer as disclosed  
25 herein. Preferably, said polypeptide is a polypeptide which is up-regulated in tissue derived from patients with pancreatic cancer. Yet it is also envisaged that non-human transgenic animals be produced which do not express marker genes as disclosed herein or who express limited amounts of said marker gene products. Said animals are preferably related to polypeptides which are down-regulated in pancreatic cancer. Transgenic non-  
30 human animals comprising and/or expressing the up-regulated polypeptides of the present invention or alternatively, which comprise silenced or less efficient versions of down-regulated polypeptides are useful models for studying the development of pancreatic cancer and provide for useful models for testing drugs and therapeutics for pancreatic cancer treatment and/or prevention.

A compound which interacts with a polypeptide listed in table 2, 3, 5 and/or 6 and which inhibits or antagonizes said polypeptide is identified by determining the activity of said polypeptide in the presence of said compound.

5       The term "activity" as used herein relates to the functional property or properties of a specific polypeptide. For the enzymes listed in table 2, 3, 5 and/or 6, the term "activity" relates to the enzymatic activity of a specific polypeptide. Activity assays for the enzymes listed in table 2, 3, 5 and/or 6 are well known.

10       For adhesion molecules listed in table 2, 3, 5 and/or 6, the term "activity" relates to the adhesive properties of a polypeptide and may be determined using assays such as, but not limited to, adhesion assays, cell spreading assays, or in vitro interaction of the adhesion molecule with a known ligand. Such assays are well known in the art.

15       For cytoskeletal proteins, the term "activity" relates to the regulation of the cytoskeleton by such polypeptides, or to their incorporation into the cytoskeleton. As a non-limiting example, the ability of Gelsolin to regulate actin polymerization, or of Filamin A to promote orthogonal branching of actin filaments, may be determined using in vitro actin polymerization assays. Activity in relation to the regulation of cytoskeletal  
20       structures may further be determined by, as non-limiting examples, cell spreading assays, cell migration assays, cell proliferation assays or immunofluorescence assays, or by staining actin filaments with fluorescently labeled phalloidin. All of these assays are well known to the person skilled in the art.

25       For ion channels (Chloride intracellular channel protein) the term "activity" relates to ion flux (Chloride flux) across the membrane. Methods to determine ion flux across membranes are well known to the person skilled in the art.

For transcription factors, eg. KIAA 1034, the term "activity" relates to their ability to regulate gene transcription. The transcriptional activity of a polypeptide can be determined using commonly used assays, such as a reporter gene assay.

5 For growth factors and hormones or their receptors, the term "activity" relates to their ability to bind to their receptors or ligands, respectively, and to induce receptor activation and subsequent signaling cascades, and/or it relates to the factor's or receptor's ability to mediate the cellular function or functions eventually caused by growth factor or hormone mediated receptor activation. Growth factor or hormone binding to receptors  
10 can be determined by commonly known ligand binding assays. Receptor activation can be determined by testing for receptor auto-phosphorylation, or by assaying for modification or recruitment of downstream signaling mediators to the receptors (by immunoprecipitation and Western Blotting of signaling complexes). Cellular functions regulated by growth factors or hormones and their receptors can be cell proliferation (eg  
15 determined by using thymidine incorporation or cell counts), cell migration assays (eg determined by using modified Boyden chambers), cell survival or apoptosis assays (eg determined by using DAPI staining), angiogenesis assays (eg in vitro assays to measure endothelial tube formation that are commercially available). In addition to these assays, other assays may be used as well to determine these and other cellular functions.

20

Inhibitors or antagonists of a polypeptide listed in tables 2 and/or 3 are identified by the screening method described above when there is a decreased activity determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor or antagonist.

25

Further to the screening methods disclosed above, this invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting a host which expresses said  
30 polypeptide with a compound; b) determining the expression level and/or activity of said polypeptide; c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the expression level of said polypeptide as determined in (b) and

(c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

5 An inhibitor of the expression of a polypeptide listed in table 2, 3, 5 and/or 6 is identified by the screening method described hereinbefore when a decreased expression of the protein is determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor of expression of a polypeptide.

10 The term "express" as used herein relates to expression levels of a polypeptide listed table 2, 3, 5 and/or 6 which is up-regulated in pancreatic cancer, in cells, preferably in a pancreatic adenocarcinoma cell line, which are elevated as compared to the expression levels of the same polypeptide in healthy pancreatic cells. Preferably, expression levels are at least 2 fold, more preferably at least 3 fold, even more preferably  
15 at least 4 fold, most preferably at least 5 fold higher than in healthy pancreatic cells.

Furthermore, the present invention provides a compound identified and/or obtained by any of the screening methods hereinbefore described. Said compound is further comprised in a pharmaceutical composition. A method for the preparation of  
20 said pharmaceutical composition comprising formulating said compound in a pharmaceutically acceptable carrier or diluent is also claimed. Any conventional carrier material can be utilized. The carrier material can be an organic or inorganic one suitable for eteral, percutaneous or parenteral administration. Suitable carriers include water, gelatin, gum arabic, lactose, starch, magnesium stearate, talc, vegetable oils, polyalkylene-  
25 glycols, petroleum jelly and the like. Furthermore, the pharmaceutical preparations may contain other pharmaceutically active agents. Additional additives such as flavoring agents, stabilizers, emulsifying agents, buffers and the like may be added in accordance with accepted practices of pharmaceutical compounding.

30 Said compound may be used for the preparation of a medicament for the treatment or prevention of pancreatic cancer. In addition, said compound may also be used for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. Preferably, said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense  
35 construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

5 In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided  
10 by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 2 and/or 3 or inhibit the expression of any of said polypeptides.

The present invention pertains to a marker for diagnosis of pancreatic cancer  
15 comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6. Preferably, said marker does not include Seq ID No.s 25 and 50 to 55. In a more preferred embodiment, said marker comprises at least one of the polypeptides listed in table 5.

The present invention also provides an in vitro method for the diagnosis of  
20 pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

- a) obtaining a biological sample; and
- b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.

Preferably, said in vitro method additionally comprises the step of detecting and/or  
25 measuring the decrease of at least one of the polypeptides listed in table 5. More preferably, in said vitro method, said at least one polypeptide does not include Seq ID No.s 25 and 50 to 55. Even more preferably, in said vitro method, said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

30

The present invention further provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

- a) obtaining a biological sample; and
- b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker hereinbefore described.

Preferably, in said in vitro method, said nucleic acid molecule is RNA or DNA.

- 5 More preferably, in said in vitro method, said DNA is a cDNA.

In a further more preferred embodiment of any of the in vitro methods hereinbefore described, the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual. In a most preferred embodiment of any of the in vitro methods  
10 hereinbefore described, the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

In a further preferred embodiment of the in vitro method hereinbefore described,  
15 an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also pertains to a screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in  
20 pancreatic cancer, comprising the steps of

- a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and
- b) detecting the interaction between said compound or plurality of compounds  
25 with said polypeptide.

Furthermore, the present invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

- a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;
- b) determining the activity of said polypeptide;
- 5 c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and
- d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

10

The present invention also provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

15

- a) contacting a host which expresses said polypeptide with a compound,
- b) determining the expression level and/or activity of said polypeptide;
- c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and
- d) quantitatively relating the expression level of said polypeptide as determined  
20 in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

20

The present invention provides a compound identified and/or obtained by the  
25 screening methods hereinbefore described.

In addition, the present invention provides a pharmaceutical composition comprising the compound hereinbefore described. Also provided is a method for the preparation of the pharmaceutical composition hereinbefore described comprising  
30 formulating the compound hereinbefore described in a pharmaceutically acceptable carrier or diluent.

30



The present invention provides a use of a compound hereinbefore described for the preparation of a medicament for the treatment or prevention of pancreatic cancer. Also provided is a use of a compound hereinbefore described for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. In a preferred embodiment, the uses hereinbefore described relate to a compound comprising an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 5 and/or 6 or inhibit the expression of any of said polypeptides.

In the present invention, the proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples are also claimed.

Examples:**Collection of tissue samples**

- 5           Pancreatic carcinomas and adjacent tissue were collected from the patients listed in table 1.

Samples were collected shortly after the resection (less than 30 minutes), and fast frozen in liquid nitrogen for about 1 minute, then stored in a freezer at a temperature of  $-80^{\circ}\text{C}$ .

10   **Characterization of formalin-fixed specimens**

Histopathological characterization was carried out by using hematoxylin-eosin-stained sections of formalin-fixed and paraffin-embedded specimens. Tumors were classified using the WHO system. The types of pancreatic carcinomas included in the study are shown in table 1.

15

- The twelve pancreatic carcinoma samples used in this study were ductal carcinomas which constitute the overwhelming proportion of pancreatic carcinomas. The patient-matched samples from histologically normal tissue surrounding the carcinoma were used as controls. We carried out 12 pairs of 2-dimensional electrophoresis maps for
- 20   comparing protein expression between tumor tissue and normal control tissue. For protein identification, the samples were pooled, thus generating pan-Carcinoma and pan-Normal protein extracts. Quantification was carried out in two steps: (I) Gels from the pooled samples were compared using the PDQuest image analysis software. (II) The changes identified at the level of the pooled samples were cross-validated by an analysis of
- 25   the individual samples. The change factors shown in table 2, 3, 5 and 6 were determined using the pooled samples.

### Preparation of samples for electrophoresis

Samples cleaned of clots and contaminating tissue were frozen in liquid nitrogen, then ground to powder. Samples were suspended in lysis buffer (8M urea, 4% CHAPS, 40mMol/L Tris-Cl, 0.5% carrier ampholytes, 100mMol/L DTT and 0.1g/l PMSF) and  
5 centrifuged at 12000rpm for 30 minutes. The supernatants were stored at -80°C. The protein concentration in the extracts was determined by the Bradford method (Bradford, M. Anal. Biochem. 72, 248 (1976)).

### Two-dimensional gel electrophoresis

10 Samples containing 1 mg of protein were loaded onto the rehydrated IPG strip (18 cm, pH3~10) by using the cup loading method. IEF was performed using Pharmacia Multiphor apparatuses under the following conditions: First, the voltage was increased 200V-5000V over 24hrs, then a constant voltage of 5000V was applied for 24 hrs, the running temperature was 20°C. After IEF, the strips were equilibrated with 10 ml  
15 equilibration solution I (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 30 mM Dithioerythritol) for 15 min, then for another 15 min with equilibration solution II (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 0.23 M Iodoacetamide).

The second dimension SDS polyacrylamide gel electrophoresis (SDS-PAGE) was  
20 carried out using a Hoefer ISO\_DALT apparatus (10 gels/run, 24×20 cm), IEF strips were loaded onto 12% homogeneous polyacrylamide gels (1.5 mm x 24 cm x 20 cm). The gels were run in TGS\_Buffer (250 mM Tris, 1.92 M Glycine, 1% (w/v) SDS, pH = 8.3, Bio-Rad) at a constant voltage (80 V, 20°C).

### 25 Gel fixation and staining

Gels were fixed in 50% Methanol/20% acetic acid for 30 min, then washed in ultra-pure water for 30 min and stained with NOVEX Colloidal Blue staining Kit (Invitrogen) following the manufacturer's recommendations.

## Protein Identification

The protein identification was performed using a two-step procedure.

### In-gel digestion

- 5 Spots were picked and transferred into 96-well by a spot picking robot. From each gel, 600-800 spots were picked. The spots were destained with 100µl of 30% acetonitrile in 50mM ammonium bicarbonate, washed in ultra pure-water and dried in a speed vac evaporator. The dry gel pieces were digested with 10ng/µl trypsin (Promega, Madison, USA) solution in 500 nM ammonium bicarbonate at room temperature for 16 h
- 10 maximum. The peptides from each spot were extracted with 20µl of 0.1% trifluoro acetic acid (TFA) in 50% acetonitrile. The matrix solution consisted of 0.025%(w/v) alpha-cyano-4-hydroxy cinammic acid (Sigma) in 50% acetonitrile/0.1% TFA with internal standard peptides des-Arg-Bradykinin(Sigma, MW 904.4681 Da) and adrenocorticotrophic hormone fragment 18-39 (Sigma, MW 2465.1989 Da).

15

### Analysis by MALDI-TOF

- 1.5ul of peptide extract and 1.0µl of matrix solution were simultaneously applied to the spots on the MS target. Recrystallization was carried out as specified by the instruments manufacturer. The samples were analyzed in a MALDI-time of flight Mass spectrometer (Autoflex, Bruker Analytics, Bremen, Germany). Peak annotation and
- 20 database search by peptide matching was performed by in house developed software. The peptide mass was compared with theoretic peptide masses of all available proteins from all species. The monoisotopic mass was used and a mass tolerance of 0.0025% was allowed. 4 matching peptides were the minimal requirement for an identity assignment.
- 25 Mismatch or miscleavage sites were not considered.

Table 1: Clinical and histopathological characteristics of samples

No. of Samples	Sex	Age	Tumor location	Histology	Metastasis in lymph nodes
PC-01	Male	48	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-02	Male	68	Head of pancreas	Poorly differentiated adenocarcinoma	Yes
PC-03	Male	44	Head of pancreas	Poorly differentiated ductal adenocarcinoma, clear cell type	Yes
PC-04	Male	66	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-05	Female	45	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-06	Female	65	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-07	Male	59	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-08	Female	62	Body of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-09	Male	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	No
PC-10	Female	53	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-11	Female	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-12	Female	69	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes

Table 2: Proteins up-regulated in pancreatic cancer I

Protein	Acc No	Description	Seq ID No.	Fold Change
sw:CATD_HUMAN	P07339	Cathepsin D precursor (ec 3.4.23.5).	1	<2
sw:IDHC_HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (ec 1.1.1.42)	2	2
sw:GELS_HUMAN	P06396	Gelsolin precursor, plasma	3	3
sw:CFAB_HUMAN	P00751	Complement factor B precursor (ec 3.4.21.47)	4	5
sw:AAC4_HUMAN	O43707	Alpha-actinin 4 (non-muscle alpha-actinin 4)	5	2
sw:AAC1_HUMAN	P12814	Alpha-actinin 1 (alpha-actinin cytoskeletal isoform)	7	2
sw:TBA4_HUMAN	P05215	Tubulin alpha-4 chain.	8	2
sw:ABP2_HUMAN	P21333	Filamin A (Endothelial actin-binding protein)	9	4
sw:TAGL_HUMAN	P37802	Transgelin 2 (smooth muscle protein 22-alpha)	10	2
sw:TPM4_HUMAN	P07226	Tropomyosin alpha 4 chain	11	<2
sw:BGH3_HUMAN	Q15582	Transforming growth factor-beta induced protein IG-H3 precursor	6	5
sw:CALD_HUMAN	Q05682	Caldesmon (cdm)	12	2
sw:ENOL_HUMAN	Q05524	Alpha enolase	13	2
sw:ACY1_HUMAN	Q03154	Aminoacylase-1	14	5
sw:CAPB_HUMAN	P47756	F-actin capping protein beta subunit (capz beta)	15	5
sw:IPYR_HUMAN	Q15181	Inorganic pyrophosphatase	16	<2
sw:LEG3_HUMAN	P17931	Galectin-3 (galactose-specific lectin 3).	17	2

sw:POR2_HUMAN	P45880	Voltage-dependent anion-selective channel protein 2	18	<2
SW:ANX2_HUMAN	P07355	Annexin II	19	2
sw:CBP2_HUMAN	P50454	Collagen-binding protein 2 precursor	20	2
sw:COF1_HUMAN	P23528	Cofilin, non-muscle isoform	21	<2
sw:CYPH_HUMAN	P05092	Peptidyl-prolyl cis-trans isomerase A	22	<2
sw:DYI2_HUMAN	Q13409	Dynein intermediate chain 2, cytosolic	23	2
sw:ECH1_HUMAN	Q13011	Delta3,5-Delta2,4-dienoyl-coa isomerase, mitochondrial precursor	24	2
sw:MLRN_HUMAN	P24844	Myosin regulatory light chain 2	48	2
sw:PLSL_HUMAN	P13796	L-Plastin	26	<2
sw:RAN_HUMAN	P17080	GTP-binding nuclear protein ran	27	3
sw:ROK_HUMAN	Q07244	Heterogeneous nuclear ribonucleoprotein k	28	2
sw:TCTP_HUMAN	P13693	Translationally controlled tumor	29	<2
sw:TPM1_HUMAN	P09493	Tropomyosin 1 alpha chain	30	<2
sw:TYPH_HUMAN	P19971	Thymidine phosphorylase precursor	31	5
sw:AMPL_HUMAN	P28838	Cytosol aminopeptidase	32	3
sw:K1CS_HUMAN	P08727	Keratin, type i cytoskeletal 19 (cytokeratin 19)	33	4
sw:ALDX_HUMAN	P14550	Alcohol dehydrogenase [NADP+]	34	4
sw:EL3A_HUMAN	P09093	Elastase IIIa precursor	35	4
sw:DLDH_HUMAN	P09622	Dihydrolipoamide dehydrogenase, mitochondrial precursor	36	2
sw:ECHM_HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial precursor	37	3
sw:HSBX_HUMAN	O14558	Heat-shock 20 kDa like-protein p20.	38	2

sw:MLEN_HUMAN	P16475	Myosin light chain alkali, non-muscle isoform	39	3
sw:CALX_HUMAN	P27824	Calnexin precursor	40	3
sw:MA32_HUMAN	Q07021	Complement component 1	41	<2
sw:NUAM_HUMAN	P28331	NADH-ubiquinone oxidoreductase 75 kda subunit, mitochondrial precursor	42	2
sw:PBEF_HUMAN	P43490	Pre-B cell enhancing factor precursor.	43	2
sw:RET1_HUMAN	P09455	Retinol-binding protein I, cellular	44	2
sw:TCPG_HUMAN	P49368	T-complex protein 1, gamma subunit	45	2
sw:RINI_HUMAN	P13489	Placental ribonuclease inhibitor	46	<2
sw:GBLP_HUMAN	P25388	Guanine nucleotide-binding protein beta subunit-like protein 12.3	47	2
sw:S109_HUMAN	P06702	Calgranulin B	49	<2



Table 3: Proteins up-regulated in pancreatic cancer II

Protein	Acc No	Description	Seq ID No	Fold Change
sw:CAPG_HUMAN	P40121	Macrophage capping protein	50	3
sw:ANX1_HUMAN	P04083	Annexin I (lipocortin I) (calpactin II)	51	4
sw:K2C7_HUMAN	P08729	Keratin, type II cytoskeletal 7	52	5
humangp:CHR13-Q15063	Q15063	Osteoblast specific factor 2 precursor	53	2
sw:TGLC_HUMAN	P21980	Protein-glutamine gamma-glutamyltransferase	54	2
sw:GDIR_HUMAN	P52565	Rho GDP-dissociation inhibitor 1	55	<2
sw:IQG1_HUMAN	P46940	Ras GTPase-activating-like protein	25	2

**Table 4. Proteins roughly classified by their involved biological processing or basic function**

<b>Protein function<sup>a</sup></b>	<b>Number<sup>b</sup></b>	<b>Percentage (%)<sup>c</sup></b>
Structural constitutural and regulation of cytoskeleton	61	20.8
Cell cycle and metabolism	74	25.3
Response to external stimulus or stress	61	20.8
Signal transduction	13	4.4
Nuclear function	18	6.1
Transport processing	19	6.5
Hemostatis	12	4.1
Cell adhesion	7	2.4
Chaperon	7	2.4
Apoptosis	3	1
Unknown function	11	3.7
Others	7	2.4
Total	293	100

**Table 5. Proteins with higher levels in normal pancreatic compared to cancer tissue**

Protein <sup>a</sup>	AccNo <sup>b</sup>	Description <sup>c</sup>	Fold <sup>d</sup>	Seq ID No.
<b>cytoskeletal regulation</b>				
sw:DESM_HUMAN	P17661	desmin.	3	70
<b>proteolysis and peptidolysis</b>				
sw:CBPB_HUMAN	P15086	carboxypeptidase b precursor	2	71
sw:CBP1_HUMAN	P15085	carboxypeptidase a1 precursor	Uncalculated	72
sw:CPB2_HUMAN	P50454	carboxypeptidase a2 precursor	Uncalculated	73
sw:CTRB_HUMAN	P17538	chymotrypsinogen b precursor	Uncalculated	74
sw:TRY1_HUMAN	P07477	trypsin i precursor (ec 3.4.21.4) (cationic trypsinogen).	Uncalculated	75
sw:TRY2_HUMAN	P07478	trypsin ii precursor (anionic trypsinogen).	3	76
sw:ILEU_HUMAN	P30740	leukocyte elastase inhibitor	4	77
<b>chaperon</b>				
sw:CH60_HUMAN	P10809	human. mitochondrial matrix protein p1 precursor	2	78
sw:ENPL_HUMAN	P14625	94 kda glucose-regulated protein	3	79
SW:ER29_HUMAN	P30040	endoplasmic reticulum protein erp29 precursor	2	80
sw:PDA2_HUMAN	Q13087	protein disulfide isomerase a2 precursor	2	81
sw:PDA3_HUMAN	P30101	protein disulfide isomerase a3 precursor	2	82
<b>oxidoreductase</b>				
sw:ADHB_HUMAN	P00325	alcohol dehydrogenase beta chain	<2	83
sw:GTO1_HUMAN	P78417	glutathione transferase omega 1	Uncalculated	84
sw:OXRP_HUMAN	Q9Y4L1	150 kda oxygen-regulated protein precursor	Uncalculated	85

- 31 -

sw:PDX4_HUMAN	Q13162	peroxiredoxin 4	<2	86
sw:ULA4_HUMAN	P30039	mawd binding protein	<2	87
metabolism of biological process				
sw:AMYC_HUMAN	P19961	alpha-amylase 2b precursor	3	88
sw:AMYP_HUMAN	P04746	alpha-amylase, pancreatic precursor	Uncalculated	89
sw:ATPA_HUMAN	P25705	atp synthase alpha chain, mitochondrial precursor	<2	90
sw:BAL_HUMAN	P19835	bile-salt-activated lipase precursor	3	91
sw:LIP1_HUMAN	P54315	pancreatic lipase related protein 1 precursor	<2	92
sw:LIP2_HUMAN	P54317	pancreatic lipase related protein 2 precursor	Uncalculated	93
sw:LIPP_HUMAN	P16233	triacylglycerol lipase, pancreatic precursor	Uncalculated	94
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		95
sw:GABT_HUMAN	P80404	4-aminobutyrate aminotransferase	2	96
sw:GATM_HUMAN	P50440	glycine amidinotransferase, mitochondrial precursor	Uncalculated	97
sw:GR78_HUMAN	P11021	78 kda glucose-regulated protein precursor (grp 78)	3	98
sw:IF32_HUMAN	Q13347	eukaryotic translation initiation factor 3 subunit 2	<2	99
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		100
sw:PGMU_HUMAN	P36871	phosphoglucomutase	2	101
sw:PSA1_HUMAN	P25786	proteasome subunit alpha type 1	2	102
heat shock protein				
sw:HS27_HUMAN	P04792	heat shock 27 kda protein	Uncalculated	103
signaling				
SW:PD6I	Q8WUM4	programmed cell death 6 interacting protein	5	104
muscle development				

- 32 -

hsugp:057687-10-0	Q9bva2	four and a half lim domains 3	<2	105
SW:sli2	Q13643	Skeletal muscle LIM-protein 2 (SLIM 2)(Four and a half LIM domains protein 3)(FHL3).	<2	106
transport of biological process				
sw:CYB5_HUMAN	P00167	cytochrome b5.	2	107
cell adhesion				
sw:PAP1_HUMAN	Q06141	pancreatitis-associated protein 1 precursor.	Uncalculated	108
other				
SW:CA16_HUMAN	P12109	collagen alpha 1(vi) chain precursor.	5	109
SW:LUM_HUMAN	P51884	lumican precursor	3	110

**Table 6 Proteins with higher levels in pancreatic cancer compared to in normal tissue**

Protein <sup>a</sup>	AccNo <sup>b</sup>	Description <sup>c</sup>	Fold <sup>d</sup>	Seq ID No.
<b>cytoskeletal regulation</b>				
sw:FSC2_HUMAN	O14926	fascin 2 (retinal fascin).	2	56
sw:AAC1_HUMAN	P12814	alpha-actinin 1	2	7
sw:AAC4_HUMAN	O43707	alpha-actinin 4	2	5
sw:ABP2_HUMAN	P21333	endothelial actin-binding protein (alpha-filamin).	4	9
sw:ANX2_HUMAN	P07355	human annexin ii (lipocortin ii)	2	19
sw:CALD_HUMAN	Q05682	caldesmon (cdm).	2	12
sw:CAPB_HUMAN	P47756	f-actin capping protein beta subunit	5	15
sw:CAPG_HUMAN	P40121	macrophage capping protein	3	50
sw:COF1_HUMAN	P23528	cofilin, non-muscle isoform (p18).	<2	21
sw:DEST_HUMAN	P18282	destrin (actin-depolymerizing factor) (adf).	2	57
sw:DYI2_HUMAN	Q13409	dynein intermediate chain 2(fragment).	2	23
sw:GELS_HUMAN	P06396	gelsolin precursor	3	3
sw:K1CS_HUMAN	P08727	keratin, type i cytoskeletal 19	4	33
sw:K2C7_HUMAN	P08729	keratin, type ii cytoskeletal 7	5	52
sw:MLEN_HUMAN	P16475	myosin light chain alkali	3	39
sw:PLSL_HUMAN	P13796	l-plastin (lymphocyte cytosolic protein 1)	<2	26
sw:TAGL_HUMAN	P37802	transgelin (22 kda actin-binding protein).	2	10
sw:TBA4_HUMAN	P05215	tubulin alpha-4 chain.	2	8
<b>proteolysis and peptidolysis</b>				
sw:ACY1_HUMAN	Q03154	aminoacylase-1	5	14
sw:AMPL_HUMAN	P28838	cytosol aminopeptidase	3	32
sw:CATD_HUMAN	P07339	cathepsin d precursor.	<2	1

- 34 -

sw:CFAB_HUMAN	P00751	complement factor b precursor	5	4
sw:EL3A_HUMAN	P09093	elastase iiii precursor	4	35
<b>chaperon</b>				
sw:APE_HUMAN	P02649	apolipoprotein e precursor (apo-e).	<2	59
sw:CALX_HUMAN	P27824	calnexin precursor(p90)	3	40
sw:CYPH_HUMAN	P05092	peptidyl-prolyl cis-trans isomerase a	<2	22
sw:TCPG_HUMAN	P49368	t-complex protein 1, gamma subunit	2	45
sw:CBP2_HUMAN	P50454	human. collagen-binding protein 2 precursor	2	20
tr_hum:Q96C61	Q96C61	hypothetical 88.6 kda protein	5	60
<b>oxidoreductase</b>				
sw:DLDH_HUMAN	P09622	dihydrolipoamide dehydrogenase	2	36
sw:IDHC_HUMAN	O75874	isocitrate dehydrogenase [nadp] cytoplasmic	2	2
sw:NUAM_HUMAN	P28331	nadh-ubiquinone oxidoreductase 75 kda subunit	2	42
<b>metabolism of biological process</b>				
sw:ALDX_HUMAN	P14550	alcohol dehydrogenase [nadp+]	4	34
sw:ECH1_HUMAN	Q13011	delta3,5-delta2,4-dienoyl-coa isomerase	2	24
sw:ECHM_HUMAN	P30084	enoyl-coa hydratase, mitochondrial precursor	3	37
sw:IPYR_HUMAN	Q15181	inorganic pyrophosphatase	<2	16
sw:TYPH_HUMAN	P19971	thymidine phosphorylase precursor	5	31
SW:ENOA_HUMAN	P06733	human alpha enolase	2	61
sw:ENOL_HUMAN	Q05524	alpha enolase, lung specific	2	13
sw:SYW_HUMAN	P23381	tryptophanyl-trna synthetase	2	62
<b>heat shock protein</b>				
sw:HSBX_HUMAN	O14558	heat-shock 20 kda like-protein p20.	2	38
<b>signaling</b>				
sw:GBLP_HUMAN	P25388	guanine nucleotide-binding protein beta subunit-like protein 12.3	2	47

- 35 -

sw:GDIR_HUMAN	P52565	rho gdp-dissociation inhibitor 1	<2	55
sw:IQG1_HUMAN	P46940	ras gtpase-activating-like protein iqgap1	2	25
sw:PBEF_HUMAN	P43490	pre-b cell enhancing factor precursor.	2	43
sw:RAN_HUMAN	P17080	gtp-binding nuclear protein ran	3	27
<b>immune response</b>				
sw:KAC_HUMAN	P01834	ig kappa chain c region.	2	63
sw:MA32_HUMAN	Q07021	pre-mrna splicing factor sf2, p32 subunit.	<2	41
<b>inflammatory reponse</b>				
sw:ANX1_HUMAN	P04083	annexin i (lipocortin i)	4	51
sw:LEG3_HUMAN	P17931	galectin-3	2	17
sw:S109_HUMAN	P06702	calgranulin b (mrp-14)	<2	49
<b>muscle development</b>				
sw:TPM1_HUMAN	P09493	tropomyosin 1 alpha chain	<2	30
sw:TPM4_HUMAN	P07226	tropomyosin alpha 4 chain	<2	11
sw:MLRN_HUMAN	P24844	myosin regulatory light chain 2	2	48
<b>transport of biological process</b>				
humangp:CHR2-Q15092	Q15092	transmembrane protein.	2	64
sw:POR2_HUMAN	P45880	voltage-dependent anion-selective channel protein 2	<2	18
sw:RET1_HUMAN	P09455	retinol-binding protein I	2	44
<b>RNA processing</b>				
humangp:CHR20-Q9P2E9	O75300	ribosome binding protein 1 (kiaa1398 protein).	<2	65
sw:RINI_HUMAN	P13489	placental ribonuclease inhibitor	<2	46
sw:ROK_HUMAN	Q07244	heterogeneous nuclear ribonucleoprotein k	2	28
<b>blood coagulation</b>				
sw:FIBG_HUMAN	P02679	fibrinogen gamma chain precursor	3	66
sw:THRB_HUMAN	P00734	prothrombin precursor	<2	67
<b>Anti-apoptosis</b>				



- 36 -

sw:TCTP_HUMAN	P13693	translationally controlled tumor protein (p23)	<2	29
cell adhesion				
humangp:CHR13-Q15063	Q15063	osteoblast specific factor 2 precursor	2	53
sw:BGH3_HUMAN	Q15582	transforming growth factor-beta induced protein	5	6
other				
sw:TGLC_HUMAN	P21980	tissue transglutaminase	2	54
sw:KPY1_HUMAN	P14618	Human pyruvate kinase, cytosolic thyroid hormone-binding protein	3	68
humangp:CHR19-Q96D15	Q96D15	Reticulocalbin 3 precursor.	2	69

Claims

1. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3.
- 5 2. The marker of claim 1 wherein the group from which at least one polypeptide is selected consists of the polypeptides listed in table 2.
3. A polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3, for use as a marker or as a component of a marker for diagnosis of pancreatic  
10 cancer and/or the susceptibility to pancreatic cancer.
4. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of
  - a) obtaining a biological sample; and
  - 15 b) detecting and/or measuring the increase of a marker of claims 1 or 2.
5. The in vitro method of claim 4, wherein the marker comprises at least two polypeptides.
- 20 6. The in vitro method of claims 4 or 5 wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.
7. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of
  - 25 a) obtaining a biological sample; and
  - b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of claims 1 or 2.

8. The in vitro method of claim 7, wherein said nucleic acid molecule is RNA or DNA.

9. The in vitro method of claim 8, wherein said DNA is a cDNA.

5

10. The in vitro method of any one of claims 7 to 9, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.

10

11. The in vitro method of any one of claims 4 to 6, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

15

12. The in vitro method of claim 11, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

13. A screening method for identifying and/or obtaining a compound which interacts  
20 with a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

25 b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

14. A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of
- 5 a) contacting a said polypeptide with a compound identified and/or obtained by the screening method of claim 13 under conditions which allow interaction of said compound with said polypeptide;
  - b) determining the activity of said polypeptide;
  - c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and
  - 10 d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.
15. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting a host which expresses said polypeptide with a compound,
  - b) determining the expression level and/or activity of said polypeptide;
  - c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and
  - 20 d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.
- 25 16. A compound identified and/or obtained by the screening methods of any one of claims 13 to 15.
17. A pharmaceutical composition comprising the compound of claim 16.

18. A method for the preparation of the pharmaceutical composition of claim 17 comprising formulating the compound of claim 16 in a pharmaceutically acceptable carrier or diluent.

5 19. Use of a compound of claim 16 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

20. Use of a compound of claim 16 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

10

21. The use of claim 19 or 20 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

15 22. Antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

23. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 22.

20

24. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 1 or 2.

25 25. A kit for screening of compounds that activate or inhibit any of the polypeptides listed in tables 2 and/or 3, or stimulate or inhibit the expression of any of said polypeptides.

26. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6.
27. The marker of claim 26, wherein said at least one polypeptide does not include Seq  
5 ID No.s 25 and 50 to 55.
28. The marker according to any one of claims 26 to 27, additionally comprising at least one of the polypeptides listed in table 5.
- 10 29. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of
- a) obtaining a biological sample; and
- b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.
- 15
30. The in vitro method of claim 29, additionally comprising the step of detecting and/or measuring the decrease of at least one of the polypeptides listed in table 5.
31. The in vitro method of claims 29 or 30, wherein said at least one polypeptide does  
20 not include Seq ID No.s 25 and 50 to 55.
32. The in vitro method of any one of claims 29 to 31, wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.
- 25
33. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

- a) obtaining a biological sample; and
  - b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of any one of claims 26 to 28.
- 5 34. The in vitro method of claim 33, wherein said nucleic acid molecule is RNA or DNA.
35. The in vitro method of claim 34, wherein said DNA is a cDNA.
- 10 36. The in vitro method of any one of claims 33 to 35, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.
- 15 37. The in vitro method of any one of claims 33 to 36, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.
- 20 38. The in vitro method of claim 37, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.
39. A screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6
- 25 whose expression is upregulated in pancreatic cancer, comprising the steps of
- a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

40. A screening method for identifying and/or obtaining a compound which is an  
5 inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;

10 b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an  
15 inhibitor or antagonist.

41. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer,  
20 comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.  
25



42. A compound identified and/or obtained by the screening methods of any one of claims 39 to 41.

43. A pharmaceutical composition comprising the compound of claim 42.

5

44. A method for the preparation of the pharmaceutical composition of claim 43 comprising formulating the compound of claim 42 in a pharmaceutically acceptable carrier or diluent.

10 45. Use of a compound of claim 42 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

46. Use of a compound of claim 42 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

15

47. The use of claim 45 or 46 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

20 48. Antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

49. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 48.

25

50. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 26 to 28.

51. A kit for screening of compounds that activate or inhibit any of the polypeptides listed in table 5 and/or 6, or stimulate or inhibit the expression of any of said polypeptides.

5

52. The kit of claim 51, wherein said polypeptides are the polypeptides listed in table 6.

53. The proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples.

10

\*\*\*

## SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Specific Markers for Pancreatic Cancer

5 <130> 21525

<160> 110

<170> PatentIn version 3.2

<210> 1

10 <211> 412

<212> PRT

<213> Homo sapiens

<220>

<221> Cathepsin D precursor

15 <222> (1)..(412)

<223> Accession No. as of 06 Dec 2002: P07339

<400> 1

Met Gln Pro Ser Ser Leu Leu Pro Leu Ala Leu Cys Leu Leu Ala Ala

20 1 5 10 15

Pro Ala Ser Ala Leu Val Arg Ile Pro Leu His Lys Phe Thr Ser Ile

20 25 30

Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val Glu Asp Leu Ile Ala

35 40 45

Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro Ala Val Thr Glu  
50 55 60  
Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr  
65 70 75 80  
5 Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe Thr Val Val Phe  
85 90 95  
Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu  
100 105 110  
Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser  
10 115 120 125  
Ser Thr Tyr Val Lys Asn Gly Thr Ser Phe Asp Ile His Tyr Gly Ser  
130 135 140  
Gly Ser Leu Ser Gly Tyr Leu Ser Gln Asp Thr Val Ser Val Pro Cys  
145 150 155 160  
15 Gln Ser Ala Ser Ser Ala Ser Ala Leu Gly Gly Val Lys Val Glu Arg  
165 170 175  
Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala  
180 185 190  
Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val  
20 195 200 205  
Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val  
210 215 220  
Asp Gln Asn Ile Phe Ser Phe Tyr Leu Ser Arg Asp Pro Asp Ala Gln  
225 230 235 240

Pro Gly Gly Glu Leu Met Leu Gly Gly Thr Asp Ser Lys Tyr Tyr Lys  
 245 250 255  
 Gly Ser Leu Ser Tyr Leu Asn Val Thr Arg Lys Ala Tyr Trp Gln Val  
 260 265 270  
 5 His Leu Asp Gln Val Glu Val Ala Ser Gly Leu Thr Leu Cys Lys Glu  
 275 280 285  
 Gly Cys Glu Ala Ile Val Asp Thr Gly Thr Ser Leu Met Val Gly Pro  
 290 295 300  
 Val Asp Glu Val Arg Glu Leu Gln Lys Ala Ile Gly Ala Val Pro Leu  
 10 305 310 315 320  
 Ile Gln Gly Glu Tyr Met Ile Pro Cys Glu Lys Val Ser Thr Leu Pro  
 325 330 335  
 Ala Ile Thr Leu Lys Leu Gly Gly Lys Gly Tyr Lys Leu Ser Pro Glu  
 340 345 350  
 15 Asp Tyr Thr Leu Lys Val Ser Gln Ala Gly Lys Thr Leu Cys Leu Ser  
 355 360 365  
 Gly Phe Met Gly Met Asp Ile Pro Pro Pro Ser Gly Pro Leu Trp Ile  
 370 375 380  
 Leu Gly Asp Val Phe Ile Gly Arg Tyr Tyr Thr Val Phe Asp Arg Asp  
 20 385 390 395 400  
 Asn Asn Arg Val Gly Phe Ala Glu Ala Ala Arg Leu  
 405 410

&lt;210&gt; 2

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; Isocitrate dehydrogenase [NADP] cytoplasmic

&lt;222&gt; (1)..(414)

&lt;223&gt; Accession No. as of 06 Dec 2002: O75874

&lt;400&gt; 2

10

Met Ser Lys Lys Ile Ser Gly Gly Ser Val Val Glu Met Gln Gly Asp

1

5

10

15

Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu Ile Phe

20

25

30

15 Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn

35

40

45

Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile

50

55

60

Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu

20 65

70

75

80

Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn

85

90

95

Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile

100

105

110

Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys Pro Ile  
115 120 125  
Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr Asp Phe  
130 135 140  
5 Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp  
145 150 155 160  
Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly  
165 170 175  
Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe  
10 180 185 190  
Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr  
195 200 205  
Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys  
210 215 220  
15 Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu  
225 230 235 240  
Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala  
245 250 255  
Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr  
20 260 265 270  
Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu  
275 280 285  
Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu  
290 295 300

6/335

Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln  
305 310 315 320  
Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp  
325 330 335  
5 Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu  
340 345 350  
Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu  
355 360 365  
Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro  
10 370 375 380  
Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys  
385 390 395 400  
Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu  
405 410

15

&lt;210&gt; 3

&lt;211&gt; 782

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Gelsolin precursor, plasma

&lt;222&gt; (1)..(782)

&lt;223&gt; Accession No. as of 06 Dec 2002: P06396



&lt;400&gt; 3

```

Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
1           5           10           15
5  Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
           20           25           30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
           35           40           45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
10      50           55           60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
65           70           75           80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
           85           90           95
15  Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
           100          105          110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
           115          120          125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
20      130          135          140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145          150          155          160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
           165          170          175

```

8/335

Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val  
180 185 190

Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu  
195 200 205

5 Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile  
210 215 220

His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala  
225 230 235 240

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala  
10 245 250 255

Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln  
260 265 270

Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala  
275 280 285

15 Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser  
290 295 300

Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro  
305 310 315 320

Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His  
20 325 330 335

Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr  
340 345 350

Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys  
355 360 365

Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly  
370 375 380

Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp  
385 390 395 400

5 Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn  
405 410 415

Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala  
420 425 430

Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln  
10 435 440 445

Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr  
450 455 460

Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr  
465 470 475 480

15 Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala  
485 490 495

Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln  
500 505 510

Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln  
20 515 520 525

Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met  
530 535 540

Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro  
545 550 555 560

10/335

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr  
565 570 575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp  
580 585 590

5 Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr  
595 600 605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val  
610 615 620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly  
10 625 630 635 640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg  
645 650 655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys  
660 665 670

15 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu  
675 680 685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp  
690 695 700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys  
20 705 710 715 720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala  
725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu  
740 745 750

Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp

755

760

765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala

770

775

780

5

&lt;210&gt; 4

&lt;211&gt; 764

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Complement factor B precursor

&lt;222&gt; (1)..(764)

&lt;223&gt; Accession No. as of 06 Dec 2002: P00751

15 &lt;400&gt; 4

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu

1

5

10

15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg

20

20

25

30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser

35

40

45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser

50

55

60

12/335

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly  
65 70 75 80  
Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala  
85 90 95  
5 Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly  
100 105 110  
Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser  
115 120 125  
Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr  
10 130 135 140  
Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn  
145 150 155 160  
Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys  
165 170 175  
15 Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser  
180 185 190  
Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly  
195 200 205  
Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr  
20 210 215 220  
Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu  
225 230 235 240  
Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln  
245 250 255

13/335

Gln Lys Arg Lys Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr  
260 265 270

Leu Val Leu Asp Gly Ser Asp Ser Ile Gly Ala Ser Asn Phe Thr Gly  
275 280 285

5 Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly  
290 295 300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile  
305 310 315 320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr  
10 325 330 335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly  
340 345 350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp  
355 360 365

15 Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile  
370 375 380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr  
385 390 395 400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys  
20 405 410 415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro  
420 425 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn  
435 440 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val  
450 455 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met  
465 470 475 480

5 Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln  
485 490 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met  
500 505 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe  
10 515 520 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu  
530 535 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn  
545 550 555 560

15 Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp  
565 570 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile  
580 585 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg  
20 595 600 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro  
610 615 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu  
625 630 635 640



15/335

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys  
645 650 655  
Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile  
660 665 670  
5 Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro  
675 680 685  
Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile  
690 695 700  
Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly  
10 705 710 715 720  
Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala  
725 730 735  
His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu  
740 745 750  
15 Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu  
755 760

&lt;210&gt; 5

20 &lt;211&gt; 911

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Alpha-actinin 4

&lt;222&gt; (1)..(911)

&lt;223&gt; Accession No. 043707

&lt;400&gt; 5

5 Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser  
1 5 10 15  
Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met  
20 25 30  
Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp  
10 35 40 45  
Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu  
50 55 60  
Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp  
65 70 75 80  
15 Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu  
85 90 95  
Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val  
100 105 110  
Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser  
20 115 120 125  
Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly  
130 135 140  
Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val  
145 150 155 160

Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys  
165 170 175

Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp  
180 185 190

5 Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu  
195 200 205

Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu  
210 215 220

Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met  
10 225 230 235 240

Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala  
245 250 255

Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln  
260 265 270

15 Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn  
275 280 285

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp  
290 295 300

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val  
20 305 310 315 320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg  
325 330 335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln  
340 345 350

18/335

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn  
355 360 365

Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn  
370 375 380

5 Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp  
385 390 395 400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu  
405 410 415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys  
10 420 425 430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp  
435 440 445

Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala  
450 455 460

15 Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu  
465 470 475 480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln  
485 490 495

Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg  
20 500 505 510

Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln  
515 520 525

Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met  
530 535 540

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile  
545 550 555 560  
Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr  
565 570 575  
5 Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys  
580 585 590  
Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser  
595 600 605  
Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu  
10 610 615 620  
Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu  
625 630 635 640  
Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser  
645 650 655  
15 Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile  
660 665 670  
Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser  
675 680 685  
His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu  
20 690 695 700  
Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe  
705 710 715 720  
Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp  
725 730 735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn  
740 745 750

Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln  
755 760 765

5 Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala  
770 775 780

Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp  
785 790 795 800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser  
10 805 810 815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile  
820 825 830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val  
835 840 845

15 Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala  
850 855 860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile  
865 870 875 880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu  
20 885 890 895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu  
900 905 910

&lt;210&gt; 6

&lt;211&gt; 683

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; Transforming growth factor-beta induced protein IG-H3 precursor

&lt;222&gt; (1)..(683)

&lt;223&gt; Accession No. as of 06 Dec 2002: Q15582

&lt;400&gt; 6

10

Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu

1 5 10 15

Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu

20 25 30

15 Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val

35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn

50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile

20 65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly

85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val

100 105 110

22/335

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu  
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser  
130 135 140

5 Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val  
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val  
165 170 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr  
10 180 185 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly  
195 200 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala  
210 215 220

15 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr  
225 230 235 240

Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu  
245 250 255

Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn  
20 260 265 270

Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile  
275 280 285

Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg  
290 295 300



Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala  
305 310 315 320  
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu  
325 330 335  
5 Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile  
340 345 350  
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp  
355 360 365  
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala  
10 370 375 380  
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu  
385 390 395 400  
Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu  
405 410 415  
15 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg  
420 425 430  
Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr  
435 440 445  
Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg  
20 450 455 460  
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala  
465 470 475 480  
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg  
485 490 495

24/335

Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp  
500 505 510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr  
515 520 525

5 Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn  
530 535 540

Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly  
545 550 555 560

Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu  
10 565 570 575

Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu  
580 585 590

Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val  
595 600 605

15 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val  
610 615 620

Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln  
625 630 635 640

Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln  
20 645 650 655

Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro  
660 665 670

Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His  
675 680

&lt;210&gt; 7

&lt;211&gt; 892

5 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Alpha-actinin 1

&lt;222&gt; (1)..(892)

10 &lt;223&gt; Accession No. P12814

&lt;400&gt; 7

Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu  
1 5 10 15  
15 Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln  
20 25 30  
Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala  
35 40 45  
Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys  
20 50 55 60  
Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro  
65 70 75 80  
Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala  
85 90 95

26/335

Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala  
 100 105 110  
 Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp  
 115 120 125  
 5 Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr  
 130 135 140  
 Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro  
 145 150 155 160  
 Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly  
 10 165 170 175  
 Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp  
 180 185 190  
 Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala  
 195 200 205  
 15 Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala  
 210 215 220  
 Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr  
 225 230 235 240  
 Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu  
 20 245 250 255  
 Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn  
 260 265 270  
 Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu  
 275 280 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn  
290 295 300  
Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg  
305 310 315 320  
5 Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile  
325 330 335  
Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala  
340 345 350  
Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp  
10 355 360 365  
Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn  
370 375 380  
Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg  
385 390 395 400  
15 Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met  
405 410 415  
Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala  
420 425 430  
Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln  
20 435 440 445  
Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu  
450 455 460  
Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys  
465 470 475 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala  
485 490 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu  
500 505 510

5 Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala  
515 520 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile  
530 535 540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp  
10 545 550 555 560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser  
565 570 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr  
580 585 590

15 Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg  
595 600 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg  
610 615 620

Gln Gln His Asn Glu Ser Val Arg Lys Gln Phe Gly Ala Gln Ala Asn  
20 625 630 635 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile  
645 650 655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg  
660 665 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu  
675 680 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys  
690 695 700

5 His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu  
705 710 715 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu  
725 730 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg  
10 740 745 750

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro  
755 760 765

Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn  
770 775 780

15 Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp  
785 790 795 800

Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met  
805 810 815

Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser  
20 820 825 830

Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu  
835 840 845

Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met  
850 855 860

30/335

Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met

865

870

875

880

Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu

885

890

5

&lt;210&gt; 8

&lt;211&gt; 448

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Tubulin alpha-4 chain

&lt;222&gt; (1)..(448)

&lt;223&gt; Accession No. P05215

15 &lt;400&gt; 8

Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln Met

1

5

10

15

Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro

20

20

25

30

Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser

35

40

45

Phe Thr Thr Phe Phe Cys Glu Thr Gly Ala Gly Lys His Val Pro Arg

50

55

60



31/335

Ala Val Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Ile Arg Asn  
65 70 75 80  
Gly Pro Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys  
85 90 95  
5 Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys  
100 105 110  
Glu Ile Ile Asp Pro Val Leu Asp Arg Ile Arg Lys Leu Ser Asp Gln  
115 120 125  
Cys Thr Gly Leu Gln Gly Phe Leu Val Phe His Ser Phe Gly Gly Gly  
10 130 135 140  
Thr Gly Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp  
145 150 155 160  
Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln  
165 170 175  
15 Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His  
180 185 190  
Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu Ala  
195 200 205  
Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr Tyr  
20 210 215 220  
Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr Ala  
225 230 235 240  
Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe Gln  
245 250 255

32/335

Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Ala Thr Tyr  
260 265 270

Ala Pro Val Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser Val  
275 280 285

5 Ala Glu Ile Thr Asn Ala Cys Phe Glu Pro Ala Asn Gln Met Val Lys  
290 295 300

Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Leu Leu Tyr Arg  
305 310 315 320

Gly Asp Val Val Pro Lys Asp Val Asn Ala Ala Ile Ala Ala Ile Lys  
10 325 330 335

Thr Lys Arg Ser Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe Lys  
340 345 350

Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp Leu  
355 360 365

15 Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala Ile  
370 375 380

Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr Ala  
385 390 395 400

Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu Gly  
20 405 410 415

Glu Phe Ser Glu Ala Arg Glu Asp Met Ala Ala Leu Glu Lys Asp Tyr  
420 425 430

Glu Glu Val Gly Ile Asp Ser Tyr Glu Asp Glu Asp Glu Gly Glu Glu  
435 440 445

<210> 9

<211> 2647

5 <212> PRT

<213> Homo sapiens

<220>

<221> Filamin A

<222> (1)..(2647)

10 <223> Accession No. P21333

<400> 9

Met Ser Ser Ser His Ser Arg Ala Gly Gln Ser Ala Ala Gly Ala Ala

1 5 10 15

15 Pro Gly Gly Gly Val Asp Thr Arg Asp Ala Glu Met Pro Ala Thr Glu

20 25 30

Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln Asn Thr

35 40 45

Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Ser Lys Arg Ile

20 50 55 60

Ala Asn Leu Gln Thr Asp Leu Ser Asp Gly Leu Arg Leu Ile Ala Leu

65 70 75 80

Leu Glu Val Leu Ser Gln Lys Lys Met His Arg Lys His Asn Gln Arg

85 90 95

34/335

Pro Thr Phe Arg Gln Met Gln Leu Glu Asn Val Ser Val Ala Leu Glu  
100 105 110

Phe Leu Asp Arg Glu Ser Ile Lys Leu Val Ser Ile Asp Ser Lys Ala  
115 120 125

5 Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp Thr Leu  
130 135 140

Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Asp Glu Glu Glu Asp  
145 150 155 160

Glu Glu Ala Lys Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly Trp Ile  
10 165 170 175

Gln Asn Lys Leu Pro Gln Leu Pro Ile Thr Asn Phe Ser Arg Asp Trp  
180 185 190

Gln Ser Gly Arg Ala Leu Gly Ala Leu Val Asp Ser Cys Ala Pro Gly  
195 200 205

15 Leu Cys Pro Asp Trp Asp Ser Trp Asp Ala Ser Lys Pro Val Thr Asn  
210 215 220

Ala Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Ile Pro Gln  
225 230 235 240

Val Ile Thr Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu His Ser  
20 245 250 255

Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys Pro Gly  
260 265 270

Ala Pro Leu Arg Pro Lys Leu Asn Pro Lys Lys Ala Arg Ala Tyr Gly  
275 280 285

Pro Gly Ile Glu Pro Thr Gly Asn Met Val Lys Lys Arg Ala Glu Phe  
290 295 300

Thr Val Glu Thr Arg Ser Ala Gly Gln Gly Glu Val Leu Val Tyr Val  
305 310 315 320

5 Glu Asp Pro Ala Gly His Gln Glu Glu Ala Lys Val Thr Ala Asn Asn  
325 330 335

Asp Lys Asn Arg Thr Phe Ser Val Trp Tyr Val Pro Glu Val Thr Gly  
340 345 350

Thr His Lys Val Thr Val Leu Phe Ala Gly Gln His Ile Ala Lys Ser  
10 355 360 365

Pro Phe Glu Val Tyr Val Asp Lys Ser Gln Gly Asp Ala Ser Lys Val  
370 375 380

Thr Ala Gln Gly Pro Gly Leu Glu Pro Ser Gly Asn Ile Ala Asn Lys  
385 390 395 400

15 Thr Thr Tyr Phe Glu Ile Phe Thr Ala Gly Ala Gly Thr Gly Glu Val  
405 410 415

Glu Val Val Ile Gln Asp Pro Met Gly Gln Lys Gly Thr Val Glu Pro  
420 425 430

Gln Leu Glu Ala Arg Gly Asp Ser Thr Tyr Arg Cys Ser Tyr Gln Pro  
20 435 440 445

Thr Met Glu Gly Val His Thr Val His Val Thr Phe Ala Gly Val Pro  
450 455 460

Ile Pro Arg Ser Pro Tyr Thr Val Thr Val Gly Gln Ala Cys Asn Pro  
465 470 475 480

36/335

Ser Ala Cys Arg Ala Val Gly Arg Gly Leu Gln Pro Lys Gly Val Arg  
485 490 495

Val Lys Glu Thr Ala Asp Phe Lys Val Tyr Thr Lys Gly Ala Gly Ser  
500 505 510

5 Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Glu Glu Arg Val  
515 520 525

Lys Gln Lys Asp Leu Gly Asp Gly Val Tyr Gly Phe Glu Tyr Tyr Pro  
530 535 540

Met Val Pro Gly Thr Tyr Ile Val Thr Ile Thr Trp Gly Gly Gln Asn  
10 545 550 555 560

Ile Gly Arg Ser Pro Phe Glu Val Lys Val Gly Thr Glu Cys Gly Asn  
565 570 575

Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Gly Gly Val Val Gly  
580 585 590

15 Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Asp Asp Val Gly Thr  
595 600 605

Leu Gly Phe Ser Val Glu Gly Pro Ser Gln Ala Lys Ile Glu Cys Asp  
610 615 620

Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp Pro Gln Glu Ala  
20 625 630 635 640

Gly Glu Tyr Ala Val His Val Leu Cys Asn Ser Glu Asp Ile Arg Leu  
645 650 655

Ser Pro Phe Met Ala Asp Ile Arg Asp Ala Pro Gln Asp Phe His Pro  
660 665 670

37/335

Asp Arg Val Lys Ala Arg Gly Pro Gly Leu Glu Lys Thr Gly Val Ala  
675 680 685

Val Asn Lys Pro Ala Glu Phe Thr Val Asp Ala Lys His Gly Gly Lys  
690 695 700

5 Ala Pro Leu Arg Val Gln Val Gln Asp Asn Glu Gly Cys Pro Val Glu  
705 710 715 720

Ala Leu Val Lys Asp Asn Gly Asn Gly Thr Tyr Ser Cys Ser Tyr Val  
725 730 735

Pro Arg Lys Pro Val Lys His Thr Ala Met Val Ser Trp Gly Gly Val  
10 740 745 750

Ser Ile Pro Asn Ser Pro Phe Arg Val Asn Val Gly Ala Gly Ser His  
755 760 765

Pro Asn Lys Val Lys Val Tyr Gly Pro Gly Val Ala Lys Thr Gly Leu  
770 775 780

15 Lys Ala His Glu Pro Thr Tyr Phe Thr Val Asp Cys Ala Glu Ala Gly  
785 790 795 800

Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro Gly Val Val Gly  
805 810 815

Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Arg Asn Asp Asn Asp  
20 820 825 830

Thr Phe Thr Val Lys Tyr Thr Pro Arg Gly Ala Gly Ser Tyr Thr Ile  
835 840 845

Met Val Leu Phe Ala Asp Gln Ala Thr Pro Thr Ser Pro Ile Arg Val  
850 855 860

38/335

Lys Val Glu Pro Ser His Asp Ala Ser Lys Val Lys Ala Glu Gly Pro  
865 870 875 880  
Gly Leu Ser Arg Thr Gly Val Glu Leu Gly Lys Pro Thr His Phe Thr  
885 890 895  
5 Val Asn Ala Lys Ala Ala Gly Lys Gly Lys Leu Asp Val Gln Phe Ser  
900 905 910  
Gly Leu Thr Lys Gly Asp Ala Val Arg Asp Val Asp Ile Ile Asp His  
915 920 925  
His Asp Asn Thr Tyr Thr Val Lys Tyr Thr Pro Val Gln Gln Gly Pro  
10 930 935 940  
Val Gly Val Asn Val Thr Tyr Gly Gly Asp Pro Ile Pro Lys Ser Pro  
945 950 955 960  
Phe Ser Val Ala Val Ser Pro Ser Leu Asp Leu Ser Lys Ile Lys Val  
965 970 975  
15 Ser Gly Leu Gly Glu Lys Val Asp Val Gly Lys Asp Gln Glu Phe Thr  
980 985 990  
Val Lys Ser Lys Gly Ala Gly Gly Gln Gly Lys Val Ala Ser Lys Ile  
995 1000 1005  
Val Gly Pro Ser Gly Ala Ala Val Pro Cys Lys Val Glu Pro Gly  
20 1010 1015 1020  
Leu Gly Ala Asp Asn Ser Val Val Arg Phe Leu Pro Arg Glu Glu  
1025 1030 1035  
Gly Pro Tyr Glu Val Glu Val Thr Tyr Asp Gly Val Pro Val Pro  
1040 1045 1050



	Gly Ser	Pro Phe	Pro Leu	Glu	Ala Val	Ala Pro	Thr	Lys Pro	Ser
	1055			1060				1065	
	Lys Val	Lys Ala	Phe Gly	Pro	Gly Leu	Gln Gly	Gly	Ser Ala	Gly
	1070			1075				1080	
5	Ser Pro	Ala Arg	Phe Thr	Ile	Asp Thr	Lys Gly	Ala	Gly Thr	Gly
	1085			1090				1095	
	Gly Leu	Gly Leu	Thr Val	Glu	Gly Pro	Cys Glu	Ala	Gln Leu	Glu
	1100			1105				1110	
	Cys Leu	Asp Asn	Gly Asp	Gly	Thr Cys	Ser Val	Ser	Tyr Val	Pro
10	1115			1120				1125	
	Thr Glu	Pro Gly	Asp Tyr	Asn	Ile Asn	Ile Leu	Phe	Ala Asp	Thr
	1130			1135				1140	
	His Ile	Pro Gly	Ser Pro	Phe	Lys Ala	His Val	Val	Pro Cys	Phe
	1145			1150				1155	
15	Asp Ala	Ser Lys	Val Lys	Cys	Ser Gly	Pro Gly	Leu	Glu Arg	Ala
	1160			1165				1170	
	Thr Ala	Gly Glu	Val Gly	Gln	Phe Gln	Val Asp	Cys	Ser Ser	Ala
	1175			1180				1185	
	Gly Ser	Ala Glu	Leu Thr	Ile	Glu Ile	Cys Ser	Glu	Ala Gly	Leu
20	1190			1195				1200	
	Pro Ala	Glu Val	Tyr Ile	Gln	Asp His	Gly Asp	Gly	Thr His	Thr
	1205			1210				1215	
	Ile Thr	Tyr Ile	Pro Leu	Cys	Pro Gly	Ala Tyr	Thr	Val Thr	Ile
	1220			1225				1230	

	Lys	Tyr	Gly	Gly	Gln	Pro	Val	Pro	Asn	Phe	Pro	Ser	Lys	Leu	Gln
	1235							1240					1245		
	Val	Glu	Pro	Ala	Val	Asp	Thr	Ser	Gly	Val	Gln	Cys	Tyr	Gly	Pro
	1250							1255					1260		
5	Gly	Ile	Glu	Gly	Gln	Gly	Val	Phe	Arg	Glu	Ala	Thr	Thr	Glu	Phe
	1265							1270					1275		
	Ser	Val	Asp	Ala	Arg	Ala	Leu	Thr	Gln	Thr	Gly	Gly	Pro	His	Val
	1280							1285					1290		
	Lys	Ala	Arg	Val	Ala	Asn	Pro	Ser	Gly	Asn	Leu	Thr	Glu	Thr	Tyr
10	1295							1300					1305		
	Val	Gln	Asp	Arg	Gly	Asp	Gly	Met	Tyr	Lys	Val	Glu	Tyr	Thr	Pro
	1310							1315					1320		
	Tyr	Glu	Glu	Gly	Leu	His	Ser	Val	Asp	Val	Thr	Tyr	Asp	Gly	Ser
	1325							1330					1335		
15	Pro	Val	Pro	Ser	Ser	Pro	Phe	Gln	Val	Pro	Val	Thr	Glu	Gly	Cys
	1340							1345					1350		
	Asp	Pro	Ser	Arg	Val	Arg	Val	His	Gly	Pro	Gly	Ile	Gln	Ser	Gly
	1355							1360					1365		
	Thr	Thr	Asn	Lys	Pro	Asn	Lys	Phe	Thr	Val	Glu	Thr	Arg	Gly	Ala
20	1370							1375					1380		
	Gly	Thr	Gly	Gly	Leu	Gly	Leu	Ala	Val	Glu	Gly	Pro	Ser	Glu	Ala
	1385							1390					1395		
	Lys	Met	Ser	Cys	Met	Asp	Asn	Lys	Asp	Gly	Ser	Cys	Ser	Val	Glu
	1400							1405					1410		

Tyr Ile Pro Tyr Glu Ala Gly Thr Tyr Ser Leu Asn Val Thr Tyr  
 1415 1420 1425  
 Gly Gly His Gln Val Pro Gly Ser Pro Phe Lys Val Pro Val His  
 1430 1435 1440  
 5 Asp Val Thr Asp Ala Ser Lys Val Lys Cys Ser Gly Pro Gly Leu  
 1445 1450 1455  
 Ser Pro Gly Met Val Arg Ala Asn Leu Pro Gln Ser Phe Gln Val  
 1460 1465 1470  
 Asp Thr Ser Lys Ala Gly Val Ala Pro Leu Gln Val Lys Val Gln  
 10 1475 1480 1485  
 Gly Pro Lys Gly Leu Val Glu Pro Val Asp Val Val Asp Asn Ala  
 1490 1495 1500  
 Asp Gly Thr Gln Thr Val Asn Tyr Val Pro Ser Arg Glu Gly Pro  
 1505 1510 1515  
 15 Tyr Ser Ile Ser Val Leu Tyr Gly Asp Glu Glu Val Pro Arg Ser  
 1520 1525 1530  
 Pro Phe Lys Val Lys Val Leu Pro Thr His Asp Ala Ser Lys Val  
 1535 1540 1545  
 Lys Ala Ser Gly Pro Gly Leu Asn Thr Thr Gly Val Pro Ala Ser  
 20 1550 1555 1560  
 Leu Pro Val Glu Phe Thr Ile Asp Ala Lys Asp Ala Gly Glu Gly  
 1565 1570 1575  
 Leu Leu Ala Val Gln Ile Thr Asp Pro Glu Gly Lys Pro Lys Lys  
 1580 1585 1590

	Thr	His	Ile	Gln	Asp	Asn	His	Asp	Gly	Thr	Tyr	Thr	Val	Ala	Tyr
	1595						1600						1605		
5	Val	Pro	Asp	Val	Thr	Gly	Arg	Tyr	Thr	Ile	Leu	Ile	Lys	Tyr	Gly
	1610						1615						1620		
	Gly	Asp	Glu	Ile	Pro	Phe	Ser	Pro	Tyr	Arg	Val	Arg	Ala	Val	Pro
	1625						1630						1635		
	Thr	Gly	Asp	Ala	Ser	Lys	Cys	Thr	Val	Thr	Val	Ser	Ile	Gly	Gly
10	1640						1645						1650		
	His	Gly	Leu	Gly	Ala	Gly	Ile	Gly	Pro	Thr	Ile	Gln	Ile	Gly	Glu
	1655						1660						1665		
	Glu	Thr	Val	Ile	Thr	Val	Asp	Thr	Lys	Ala	Ala	Gly	Lys	Gly	Lys
	1670						1675						1680		
15	Val	Thr	Cys	Thr	Val	Cys	Thr	Pro	Asp	Gly	Ser	Glu	Val	Asp	Val
	1685						1690						1695		
	Asp	Val	Val	Glu	Asn	Glu	Asp	Gly	Thr	Phe	Asp	Ile	Phe	Tyr	Thr
	1700						1705						1710		
	Ala	Pro	Gln	Pro	Gly	Lys	Tyr	Val	Ile	Cys	Val	Arg	Phe	Gly	Gly
20	1715						1720						1725		
	Glu	His	Val	Pro	Asn	Ser	Pro	Phe	Gln	Val	Thr	Ala	Leu	Ala	Gly
	1730						1735						1740		
	Asp	Gln	Pro	Ser	Val	Gln	Pro	Pro	Leu	Arg	Ser	Gln	Gln	Leu	Ala
	1745						1750						1755		

	Pro Gln	Tyr Thr	Tyr Ala	Gln Gly	Gly Gln	Gln Thr	Trp Ala	Pro
	1760			1765			1770	
	Glu Arg	Pro Leu	Val Gly	Val Asn	Gly Leu	Asp Val	Thr Ser	Leu
	1775			1780			1785	
5	Arg Pro	Phe Asp	Leu Val	Ile Pro	Phe Thr	Ile Lys	Lys Gly	Glu
	1790			1795			1800	
	Ile Thr	Gly Glu	Val Arg	Met Pro	Ser Gly	Lys Val	Ala Gln	Pro
	1805			1810			1815	
	Thr Ile	Thr Asp	Asn Lys	Asp Gly	Thr Val	Thr Val	Arg Tyr	Ala
10	1820			1825			1830	
	Pro Ser	Glu Ala	Gly Leu	His Glu	Met Asp	Ile Arg	Tyr Asp	Asn
	1835			1840			1845	
	Met His	Ile Pro	Gly Ser	Pro Leu	Gln Phe	Tyr Val	Asp Tyr	Val
	1850			1855			1860	
15	Asn Cys	Gly His	Val Thr	Ala Tyr	Gly Pro	Gly Leu	Thr His	Gly
	1865			1870			1875	
	Val Val	Asn Lys	Pro Ala	Thr Phe	Thr Val	Asn Thr	Lys Asp	Ala
	1880			1885			1890	
	Gly Glu	Gly Gly	Leu Ser	Leu Ala	Ile Glu	Gly Pro	Ser Lys	Ala
20	1895			1900			1905	
	Glu Ile	Ser Cys	Thr Asp	Asn Gln	Asp Gly	Thr Cys	Ser Val	Ser
	1910			1915			1920	
	Tyr Leu	Pro Val	Leu Pro	Gly Asp	Tyr Ser	Ile Leu	Val Lys	Tyr
	1925			1930			1935	

	Asn	Glu	Gln	His	Val	Pro	Gly	Ser	Pro	Phe	Thr	Ala	Arg	Val	Thr
	1940						1945						1950		
	Gly	Asp	Asp	Ser	Met	Arg	Met	Ser	His	Leu	Lys	Val	Gly	Ser	Ala
	1955						1960						1965		
5	Ala	Asp	Ile	Pro	Ile	Asn	Ile	Ser	Glu	Thr	Asp	Leu	Ser	Leu	Leu
	1970						1975						1980		
	Thr	Ala	Thr	Val	Val	Pro	Pro	Ser	Gly	Arg	Glu	Glu	Pro	Cys	Leu
	1985						1990						1995		
	Leu	Lys	Arg	Leu	Arg	Asn	Gly	His	Val	Gly	Ile	Ser	Phe	Val	Pro
10	2000						2005						2010		
	Lys	Glu	Thr	Gly	Glu	His	Leu	Val	His	Val	Lys	Lys	Asn	Gly	Gln
	2015						2020						2025		
	His	Val	Ala	Ser	Ser	Pro	Ile	Pro	Val	Val	Ile	Ser	Gln	Ser	Glu
	2030						2035						2040		
15	Ile	Gly	Asp	Ala	Ser	Arg	Val	Arg	Val	Ser	Gly	Gln	Gly	Leu	His
	2045						2050						2055		
	Glu	Gly	His	Thr	Phe	Glu	Pro	Ala	Glu	Phe	Ile	Ile	Asp	Thr	Arg
	2060						2065						2070		
	Asp	Ala	Gly	Tyr	Gly	Gly	Leu	Ser	Leu	Ser	Ile	Glu	Gly	Pro	Ser
20	2075						2080						2085		
	Lys	Val	Asp	Ile	Asn	Thr	Glu	Asp	Leu	Glu	Asp	Gly	Thr	Cys	Arg
	2090						2095						2100		
	Val	Thr	Tyr	Cys	Pro	Thr	Glu	Pro	Gly	Asn	Tyr	Ile	Ile	Asn	Ile
	2105						2110						2115		

	Lys Phe	Ala Asp	Gln His	Val	Pro Gly	Ser Pro	Phe	Ser Val	Lys
	2120			2125			2130		
	Val Thr	Gly Glu	Gly Arg	Val	Lys Glu	Ser Ile	Thr	Arg Arg	Arg
	2135			2140			2145		
5	Arg Ala	Pro Ser	Val Ala	Asn	Val Gly	Ser His	Cys	Asp Leu	Ser
	2150			2155			2160		
	Leu Lys	Ile Pro	Glu Ile	Ser	Ile Gln	Asp Met	Thr	Ala Gln	Val
	2165			2170			2175		
	Thr Ser	Pro Ser	Gly Lys	Thr	His Glu	Ala Glu	Ile	Val Glu	Gly
10	2180			2185			2190		
	Glu Asn	His Thr	Tyr Cys	Ile	Arg Phe	Val Pro	Ala	Glu Met	Gly
	2195			2200			2205		
	Thr His	Thr Val	Ser Val	Lys	Tyr Lys	Gly Gln	His	Val Pro	Gly
	2210			2215			2220		
15	Ser Pro	Phe Gln	Phe Thr	Val	Gly Pro	Leu Gly	Glu	Gly Gly	Ala
	2225			2230			2235		
	His Lys	Val Arg	Ala Gly	Gly	Pro Gly	Leu Glu	Arg	Ala Glu	Ala
	2240			2245			2250		
	Gly Val	Pro Ala	Glu Phe	Ser	Ile Trp	Thr Arg	Glu	Ala Gly	Ala
20	2255			2260			2265		
	Gly Gly	Leu Ala	Ile Ala	Val	Glu Gly	Pro Ser	Lys	Ala Glu	Ile
	2270			2275			2280		
	Ser Phe	Glu Asp	Arg Lys	Asp	Gly Ser	Cys Gly	Val	Ala Tyr	Val
	2285			2290			2295		

	Val	Gln	Glu	Pro	Gly	Asp	Tyr	Glu	Val	Ser	Val	Lys	Phe	Asn	Glu
	2300						2305					2310			
	Glu	His	Ile	Pro	Asp	Ser	Pro	Phe	Val	Val	Pro	Val	Ala	Ser	Pro
	2315						2320					2325			
5	Ser	Gly	Asp	Ala	Arg	Arg	Leu	Thr	Val	Ser	Ser	Leu	Gln	Glu	Ser
	2330						2335					2340			
	Gly	Leu	Lys	Val	Asn	Gln	Pro	Ala	Ser	Phe	Ala	Val	Ser	Leu	Asn
	2345						2350					2355			
	Gly	Ala	Lys	Gly	Ala	Ile	Asp	Ala	Lys	Val	His	Ser	Pro	Ser	Gly
10	2360						2365					2370			
	Ala	Leu	Glu	Glu	Cys	Tyr	Val	Thr	Glu	Ile	Asp	Gln	Asp	Lys	Tyr
	2375						2380					2385			
	Ala	Val	Arg	Phe	Ile	Pro	Arg	Glu	Asn	Gly	Val	Tyr	Leu	Ile	Asp
	2390						2395					2400			
15	Val	Lys	Phe	Asn	Gly	Thr	His	Ile	Pro	Gly	Ser	Pro	Phe	Lys	Ile
	2405						2410					2415			
	Arg	Val	Gly	Glu	Pro	Gly	His	Gly	Gly	Asp	Pro	Gly	Leu	Val	Ser
	2420						2425					2430			
	Ala	Tyr	Gly	Ala	Gly	Leu	Glu	Gly	Gly	Val	Thr	Gly	Asn	Pro	Ala
20	2435						2440					2445			
	Glu	Phe	Val	Val	Asn	Thr	Ser	Asn	Ala	Gly	Ala	Gly	Ala	Leu	Ser
	2450						2455					2460			
	Val	Thr	Ile	Asp	Gly	Pro	Ser	Lys	Val	Lys	Met	Asp	Cys	Gln	Glu
	2465						2470					2475			



	Cys	Pro	Glu	Gly	Tyr	Arg	Val	Thr	Tyr	Thr	Pro	Met	Ala	Pro	Gly
	2480						2485						2490		
	Ser	Tyr	Leu	Ile	Ser	Ile	Lys	Tyr	Gly	Gly	Pro	Tyr	His	Ile	Gly
	2495						2500						2505		
5	Gly	Ser	Pro	Phe	Lys	Ala	Lys	Val	Thr	Gly	Pro	Arg	Leu	Val	Ser
	2510						2515						2520		
	Asn	His	Ser	Leu	His	Glu	Thr	Ser	Ser	Val	Phe	Val	Asp	Ser	Leu
	2525						2530						2535		
	Thr	Lys	Ala	Thr	Cys	Ala	Pro	Gln	His	Gly	Ala	Pro	Gly	Pro	Gly
10	2540						2545						2550		
	Pro	Ala	Asp	Ala	Ser	Lys	Val	Val	Ala	Lys	Gly	Leu	Gly	Leu	Ser
	2555						2560						2565		
	Lys	Ala	Tyr	Val	Gly	Gln	Lys	Ser	Ser	Phe	Thr	Val	Asp	Cys	Ser
	2570						2575						2580		
15	Lys	Ala	Gly	Asn	Asn	Met	Leu	Leu	Val	Gly	Val	His	Gly	Pro	Arg
	2585						2590						2595		
	Thr	Pro	Cys	Glu	Glu	Ile	Leu	Val	Lys	His	Val	Gly	Ser	Arg	Leu
	2600						2605						2610		
	Tyr	Ser	Val	Ser	Tyr	Leu	Leu	Lys	Asp	Lys	Gly	Glu	Tyr	Thr	Leu
20	2615						2620						2625		
	Val	Val	Lys	Trp	Gly	His	Glu	His	Ile	Pro	Gly	Ser	Pro	Tyr	Arg
	2630						2635						2640		
	Val	Val	Val	Pro											
	2645														

<210> 10

<211> 199

5 <212> PRT

<213> Homo sapiens

<220>

<221> Transgelin 2

<222> (1)..(199)

10 <223> Accession No. as of 06 Dec 2002: P37802

<400> 10

Met Ala Asn Arg Gly Pro Ala Tyr Gly Leu Ser Arg Glu Val Gln Gln

1                      5                      10                      15

15 Lys Ile Glu Lys Gln Tyr Asp Ala Asp Leu Glu Gln Ile Leu Ile Gln

20                      25                      30

Trp Ile Thr Thr Gln Cys Arg Lys Asp Val Gly Arg Pro Gln Pro Gly

35                      40                      45

Arg Glu Asn Phe Gln Asn Trp Leu Lys Asp Gly Thr Val Leu Cys Glu

20              50                      55                      60

Leu Ile Asn Ala Leu Tyr Pro Glu Gly Gln Ala Pro Val Lys Lys Ile

65                      70                      75                      80

Gln Ala Ser Thr Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe

85

90

95

49/335

Leu Gln Ala Ala Glu Arg Tyr Gly Ile Asn Thr Thr Asp Ile Phe Gln  
100 105 110  
Thr Val Asp Leu Trp Glu Gly Lys Asn Met Ala Cys Val Gln Arg Thr  
115 120 125  
5 Leu Met Asn Leu Gly Gly Leu Ala Val Ala Arg Asp Asp Gly Leu Phe  
130 135 140  
Ser Gly Asp Pro Asn Trp Phe Pro Lys Lys Ser Lys Glu Asn Pro Arg  
145 150 155 160  
Asn Phe Ser Asp Asn Gln Leu Gln Glu Gly Lys Asn Val Ile Gly Leu  
10 165 170 175  
Gln Met Gly Thr Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr  
180 185 190  
Gly Met Pro Arg Gln Ile Leu  
195

15

&lt;210&gt; 11

&lt;211&gt; 248

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Tropomyosin alpha 4 chain

&lt;222&gt; (1)..(248)

&lt;223&gt; Accession No. P07226

&lt;400&gt; 11

Met Ala Gly Leu Asn Ser Leu Glu Ala Val Lys Arg Lys Ile Gln Ala  
1 5 10 15  
5 Leu Gln Gln Gln Ala Asp Glu Ala Glu Asp Arg Ala Gln Gly Leu Gln  
20 25 30  
Arg Glu Leu Asp Gly Glu Arg Glu Arg Arg Glu Lys Ala Glu Gly Asp  
35 40 45  
Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Val Glu Glu Glu Leu Asp  
10 50 55 60  
Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala  
65 70 75 80  
Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn  
85 90 95  
15 Arg Ala Met Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu  
100 105 110  
Lys Glu Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu  
115 120 125  
Val Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu  
20 130 135 140  
Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu Glu  
145 150 155 160  
Leu Lys Asn Val Thr Asn Asn Leu Lys Ser Leu Glu Ala Ala Ser Glu  
165 170 175

51/335

Lys Tyr Ser Glu Lys Glu Asp Lys Tyr Glu Glu Glu Ile Lys Leu Leu

180

185

190

Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe Ala Glu Arg

195

200

205

5 Thr Val Ala Lys Leu Glu Lys Thr Ile Asp Asp Leu Glu Glu Lys Leu

210

215

220

Ala Gln Ala Lys Glu Glu Asn Val Gly Leu His Gln Thr Leu Asp Gln

225

230

235

240

Thr Leu Asn Glu Leu Asn Cys Ile

10

245

&lt;210&gt; 12

&lt;211&gt; 793

15 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Caldesmon

&lt;222&gt; (1) .. (793)

20 &lt;223&gt; Accession No. as of 06 Dec 2002: Q05682

&lt;400&gt; 12

Met Asp Asp Phe Glu Arg Arg Arg Glu Leu Arg Arg Gln Lys Arg Glu

1

5

10

15

52/335

Glu Met Arg Leu Glu Ala Glu Arg Ile Ala Tyr Gln Arg Asn Asp Asp  
20 25 30  
Asp Glu Glu Glu Ala Ala Arg Glu Arg Arg Arg Ala Arg Gln Glu  
35 40 45  
5 Arg Leu Arg Gln Lys Gln Glu Glu Glu Ser Leu Gly Gln Val Thr Asp  
50 55 60  
Gln Val Glu Val Asn Ala Gln Asn Ser Val Pro Asp Glu Glu Ala Lys  
65 70 75 80  
Thr Thr Thr Thr Asn Thr Gln Val Glu Gly Asp Asp Glu Ala Ala Phe  
10 85 90 95  
Leu Glu Arg Leu Ala Arg Arg Glu Glu Arg Arg Gln Lys Arg Leu Gln  
100 105 110  
Glu Ala Leu Glu Arg Gln Lys Glu Phe Asp Pro Thr Ile Thr Asp Ala  
115 120 125  
15 Ser Leu Ser Leu Pro Ser Arg Arg Met Gln Asn Asp Thr Ala Glu Asn  
130 135 140  
Glu Thr Thr Glu Lys Glu Glu Lys Ser Glu Ser Arg Gln Glu Arg Tyr  
145 150 155 160  
Glu Ile Glu Glu Thr Glu Thr Val Thr Lys Ser Tyr Gln Lys Asn Asp  
20 165 170 175  
Trp Arg Asp Ala Glu Glu Asn Lys Lys Glu Asp Lys Glu Lys Glu Glu  
180 185 190  
Glu Glu Glu Glu Lys Pro Lys Arg Gly Ser Ile Gly Glu Asn Gln Val  
195 200 205

Glu Val Met Val Glu Glu Lys Thr Thr Glu Ser Gln Glu Glu Thr Val  
210 215 220  
Val Met Ser Leu Lys Asn Gly Gln Ile Ser Ser Glu Glu Pro Lys Gln  
225 230 235 240  
5 Glu Glu Glu Arg Glu Gln Gly Ser Asp Glu Ile Ser His His Glu Lys  
245 250 255  
Met Glu Glu Glu Asp Lys Glu Arg Ala Glu Ala Glu Arg Ala Arg Leu  
260 265 270  
Glu Ala Glu Glu Arg Glu Arg Ile Lys Ala Glu Gln Asp Lys Lys Ile  
10 275 280 285  
Ala Asp Glu Arg Ala Arg Ile Glu Ala Glu Glu Lys Ala Ala Ala Gln  
290 295 300  
Glu Arg Glu Arg Arg Glu Ala Glu Glu Arg Glu Arg Met Arg Glu Glu  
305 310 315 320  
15 Glu Lys Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys  
325 330 335  
Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala  
340 345 350  
Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala Ala Glu  
20 355 360 365  
Glu Arg Gln Arg Ala Arg Ala Glu Glu Glu Glu Lys Ala Lys Val Glu  
370 375 380  
Glu Gln Lys Arg Asn Lys Gln Leu Glu Glu Lys Lys Arg Ala Met Gln  
385 390 395 400

54/335

Glu Thr Lys Ile Lys Gly Glu Lys Val Glu Gln Lys Ile Glu Gly Lys  
 405 410 415  
 Trp Val Asn Glu Lys Lys Ala Gln Glu Asp Lys Leu Gln Thr Ala Val  
 420 425 430  
 5 Leu Lys Lys Gln Gly Glu Glu Lys Gly Thr Lys Val Gln Ala Lys Arg  
 435 440 445  
 Glu Lys Leu Gln Glu Asp Lys Pro Thr Phe Lys Lys Glu Glu Ile Lys  
 450 455 460  
 Asp Glu Lys Ile Lys Lys Asp Lys Glu Pro Lys Glu Glu Val Lys Ser  
 10 465 470 475 480  
 Phe Met Asp Arg Lys Lys Gly Phe Thr Glu Val Lys Ser Gln Asn Gly  
 485 490 495  
 Glu Phe Met Thr His Lys Leu Lys His Thr Glu Asn Thr Phe Ser Arg  
 500 505 510  
 15 Pro Gly Gly Arg Ala Ser Val Asp Thr Lys Glu Ala Glu Gly Ala Pro  
 515 520 525  
 Gln Val Glu Ala Gly Lys Arg Leu Glu Glu Leu Arg Arg Arg Arg Gly  
 530 535 540  
 Glu Thr Glu Ser Glu Glu Phe Glu Lys Leu Lys Gln Lys Gln Gln Glu  
 20 545 550 555 560  
 Ala Ala Leu Glu Leu Glu Glu Leu Lys Lys Lys Arg Glu Glu Arg Arg  
 565 570 575  
 Lys Val Leu Glu Glu Glu Glu Gln Arg Arg Lys Gln Glu Glu Ala Asp  
 580 585 590



Arg Lys Leu Arg Glu Glu Glu Glu Lys Arg Arg Leu Lys Glu Glu Ile  
595 600 605  
Glu Arg Arg Arg Ala Glu Ala Ala Glu Lys Arg Gln Lys Met Pro Glu  
610 615 620  
5 Asp Gly Leu Ser Asp Asp Lys Lys Pro Phe Lys Cys Phe Thr Pro Lys  
625 630 635 640  
Gly Ser Ser Leu Lys Ile Glu Glu Arg Ala Glu Phe Leu Asn Lys Ser  
645 650 655  
Val Gln Lys Ser Ser Gly Val Lys Ser Thr His Gln Ala Ala Ile Val  
10 660 665 670  
Ser Lys Ile Asp Ser Arg Leu Glu Gln Tyr Thr Ser Ala Ile Glu Gly  
675 680 685  
Thr Lys Ser Ala Lys Pro Thr Lys Pro Ala Ala Ser Asp Leu Pro Val  
690 695 700  
15 Pro Ala Glu Gly Val Arg Asn Ile Lys Ser Met Trp Glu Lys Gly Asn  
705 710 715 720  
Val Phe Ser Ser Pro Thr Ala Ala Gly Thr Pro Asn Lys Glu Thr Ala  
725 730 735  
Gly Leu Lys Val Gly Val Ser Ser Arg Ile Asn Glu Trp Leu Thr Lys  
20 740 745 750  
Thr Pro Asp Gly Asn Lys Ser Pro Ala Pro Lys Pro Ser Asp Leu Arg  
755 760 765  
Pro Gly Asp Val Ser Ser Lys Arg Asn Leu Trp Glu Lys Gln Ser Val  
770 775 780

56/335

Asp Lys Val Thr Ser Pro Thr Lys Val

785

790

5 &lt;210&gt; 13

&lt;211&gt; 458

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

10 &lt;221&gt; Alpha enolase

&lt;222&gt; (1)..(458)

&lt;223&gt; Accession No. as of 06 Dec 2002: Q05524

&lt;400&gt; 13

15 Met Ser Ile Leu Lys Ile Ile His Ala Arg Asp Ile Phe Glu Ser Arg

1

5

10

15

Gly Asn Pro Thr Val Glu Val Asp Leu Tyr Thr Asn Lys Gly Gly Leu

20

25

30

Phe Gly Arg Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu

20

35

40

45

Ala Leu Leu Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Gly

50

55

60

Lys Gly Val Ser Lys Ala Val Glu His Ile Ile Asn Lys Thr Ile Ala

65

70

75

80

57/335

Pro Ala Leu Ile Ser Lys Asn Val Asn Val Val Glu Gln Asp Lys Ile  
85 90 95

Asp Asn Leu Met Leu Asp Met Asp Gly Ser Glu Asn Lys Ser Lys Phe  
100 105 110

5 Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala Val Cys Ser Asn Ala  
115 120 125

Gly Ala Thr Ala Glu Lys Gly Val Pro Leu Tyr Arg His Ile Ala Asp  
130 135 140

Leu Ala Gly Asn Asn Pro Glu Val Ile Leu Pro Val Pro Ala Phe Asn  
10 145 150 155 160

Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu  
165 170 175

Phe Met Ile Pro Pro Cys Gly Ala Asp Arg Phe Asn Asp Ala Ile Arg  
180 185 190

15 Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys Glu Lys  
195 200 205

Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro  
210 215 220

Asn Ile Leu Glu Asn Lys Glu Ala Leu Glu Leu Leu Lys Thr Ala Ile  
20 225 230 235 240

Gly Lys Ala Gly Tyr Ser Asp Lys Val Val Ile Gly Met Asp Val Ala  
245 250 255

Ala Ser Glu Phe Tyr Arg Asp Gly Lys Tyr Asp Leu Asp Phe Asn Ser  
260 265 270

Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala Asp Leu  
275 280 285

Tyr Lys Gly Phe Val Leu Gly His Ala Val Lys Asn Tyr Pro Val Gly  
290 295 300

5 Val Ser Ile Glu Asp Pro Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp  
305 310 315 320

Lys Lys Leu Phe Thr Gly Ser Leu Val Gly Ile Gln Val Val Gly Asp  
325 330 335

Asp Leu Thr Val Thr Lys Pro Glu Ala Arg Ile Ala Lys Ala Val Glu  
10 340 345 350

Glu Val Lys Ala Cys Asn Cys Leu Leu Leu Leu Lys Val Asn Gln Ile  
355 360 365

Gly Ser Val Thr Glu Ser Leu Gln Ala Cys Lys Leu Ala Gln Ser Asn  
370 375 380

15 Gly Trp Gly Val Met Pro Val Ser His Arg Leu Ser Gly Glu Thr Glu  
385 390 395 400

Asp Thr Phe Met Ala Asp Leu Val Val Gly Leu Cys Thr Gly Gln Ile  
405 410 415

Lys Thr Gly Pro Thr Cys Arg Ser Glu Arg Leu Ala Lys Tyr Asn Gln  
20 420 425 430

Leu Leu Arg Ile Glu Glu Ala Glu Ala Gly Ser Lys Ala Arg Phe Ala  
435 440 445

Gly Arg Asn Phe Arg Asn Pro Arg Ile Asn  
450 455

<210> 14  
<211> 408  
5 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Aminoacylase-1  
<222> (1)..(408)  
10 <223> Accession No. as of 06 Dec 2002: Q03154  
<400> 14

Met Thr Ser Lys Gly Pro Glu Glu Glu His Pro Ser Val Thr Leu Phe  
1 5 10 15  
15 Arg Gln Tyr Leu Arg Ile Arg Thr Val Gln Pro Lys Pro Asp Tyr Gly  
20 25 30  
Ala Ala Val Ala Phe Phe Glu Glu Thr Ala Arg Gln Leu Gly Leu Gly  
35 40 45  
Cys Gln Lys Val Glu Val Ala Pro Gly Tyr Val Val Thr Val Leu Thr  
20 50 55 60  
Trp Pro Gly Thr Asn Pro Thr Leu Ser Ser Ile Leu Leu Asn Ser His  
65 70 75 80  
Thr Asp Val Val Pro Val Phe Lys Glu His Trp Ser His Asp Pro Phe  
85 90 95

60/335

Glu Ala Phe Lys Asp Ser Glu Gly Tyr Ile Tyr Ala Arg Gly Ala Gln  
100 105 110

Asp Met Lys Cys Val Ser Ile Gln Tyr Leu Glu Ala Val Arg Arg Leu  
115 120 125

5 Lys Val Glu Gly His Arg Phe Pro Arg Thr Ile His Met Thr Phe Val  
130 135 140

Pro Asp Glu Glu Val Gly Gly His Gln Gly Met Glu Leu Phe Val Gln  
145 150 155 160

Arg Pro Glu Phe His Ala Leu Arg Ala Gly Phe Ala Leu Asp Glu Gly  
10 165 170 175

Ile Ala Asn Pro Thr Asp Ala Phe Thr Val Phe Tyr Ser Glu Arg Ser  
180 185 190

Pro Trp Trp Val Arg Val Thr Ser Thr Gly Arg Pro Gly His Ala Ser  
195 200 205

15 Arg Phe Met Glu Asp Thr Ala Ala Glu Lys Leu His Lys Val Val Asn  
210 215 220

Ser Ile Leu Ala Phe Arg Glu Lys Glu Trp Gln Arg Leu Gln Ser Asn  
225 230 235 240

Pro His Leu Lys Glu Gly Ser Val Thr Ser Val Asn Leu Thr Lys Leu  
20 245 250 255

Glu Gly Gly Val Ala Tyr Asn Val Ile Pro Ala Thr Met Ser Ala Ser  
260 265 270

Phe Asp Phe Arg Val Ala Pro Asp Val Asp Phe Lys Ala Phe Glu Glu  
275 280 285

61/335

Gln Leu Gln Ser Trp Cys Gln Ala Ala Gly Glu Gly Val Thr Leu Glu  
290 295 300  
Phe Ala Gln Lys Trp Met His Pro Gln Val Thr Pro Thr Asp Asp Ser  
305 310 315 320  
5 Asn Pro Trp Trp Ala Ala Phe Ser Arg Val Cys Lys Asp Met Asn Leu  
325 330 335  
Thr Leu Glu Pro Glu Ile Met Pro Ala Ala Thr Asp Asn Arg Tyr Ile  
340 345 350  
Arg Ala Val Gly Val Pro Ala Leu Gly Phe Ser Pro Met Asn Arg Thr  
10 355 360 365  
Pro Val Leu Leu His Asp His Asp Glu Arg Leu His Glu Ala Val Phe  
370 375 380  
Leu Arg Gly Val Asp Ile Tyr Thr Arg Leu Leu Pro Ala Leu Ala Ser  
385 390 395 400  
15 Val Pro Ala Leu Pro Ser Asp Ser  
405

&lt;210&gt; 15

20 &lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; F-actin capping protein beta subunit

&lt;222&gt; (1)..(277)

&lt;223&gt; Accession No. as of 06 Dec 2002: P47756

&lt;400&gt; 15

5 Met Ser Asp Gln Gln Leu Asp Cys Ala Leu Asp Leu Met Arg Arg Leu  
1 5 10 15  
Pro Pro Gln Gln Ile Glu Lys Asn Leu Ser Asp Leu Ile Asp Leu Val  
20 25 30  
Pro Ser Leu Cys Glu Asp Leu Leu Ser Ser Val Asp Gln Pro Leu Lys  
10 35 40 45  
Ile Ala Arg Asp Lys Val Val Gly Lys Asp Tyr Leu Leu Cys Asp Tyr  
50 55 60  
Asn Arg Asp Gly Asp Ser Tyr Arg Ser Pro Trp Ser Asn Lys Tyr Asp  
65 70 75 80  
15 Pro Pro Leu Glu Asp Gly Ala Met Pro Ser Ala Arg Leu Arg Lys Leu  
85 90 95  
Glu Val Glu Ala Asn Asn Ala Phe Asp Gln Tyr Arg Asp Leu Tyr Phe  
100 105 110  
Glu Gly Gly Val Ser Ser Val Tyr Leu Trp Asp Leu Asp His Gly Phe  
20 115 120 125  
Ala Gly Val Ile Leu Ile Lys Lys Ala Gly Asp Gly Ser Lys Lys Ile  
130 135 140  
Lys Gly Cys Trp Asp Ser Ile His Val Val Glu Val Gln Glu Lys Ser  
145 150 155 160



63/335

Ser Gly Arg Thr Ala His Tyr Lys Leu Thr Ser Thr Val Met Leu Trp  
165 170 175  
Leu Gln Thr Asn Lys Ser Gly Ser Gly Thr Met Asn Leu Gly Gly Ser  
180 185 190  
5 Leu Thr Arg Gln Met Glu Lys Asp Glu Thr Val Ser Asp Cys Ser Pro  
195 200 205  
His Ile Ala Asn Ile Gly Arg Leu Val Glu Asp Met Glu Asn Lys Ile  
210 215 220  
Arg Ser Thr Leu Asn Glu Ile Tyr Phe Gly Lys Thr Lys Asp Ile Val  
10 225 230 235 240  
Asn Gly Leu Arg Ser Ile Asp Ala Ile Pro Asp Asn Gln Lys Phe Lys  
245 250 255  
Gln Leu Gln Arg Glu Leu Ser Gln Val Leu Thr Gln Arg Gln Ile Tyr  
260 265 270  
15 Ile Gln Pro Asp Asn  
275

&lt;210&gt; 16

20 &lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Inorganic pyrophosphatase

&lt;222&gt; (1) .. (289)

&lt;223&gt; Accession No. as of 06 Dec 2002: Q15181

&lt;400&gt; 16

5 Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu  
1 5 10 15  
Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe  
20 25 30  
His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val  
10 35 40 45  
Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp  
50 55 60  
Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr  
65 70 75 80  
15 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala  
85 90 95  
Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly  
100 105 110  
Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys  
20 115 120 125  
Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu  
130 135 140  
Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn  
145 150 155 160

65/335

Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys  
165 170 175  
Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg  
180 185 190  
5 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala  
195 200 205  
Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His  
210 215 220  
Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile  
10 225 230 235 240  
Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro  
245 250 255  
Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser  
260 265 270  
15 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys  
275 280 285  
Asn

20

&lt;210&gt; 17

&lt;211&gt; 250

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Galectin-3 (Galactose-specific lectin 3)

&lt;222&gt; (1)..(250)

&lt;223&gt; Accession No. as of 06 Dec 2002: P17931

5 &lt;400&gt; 17

Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn  
1 5 10 15  
Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly  
10 20 25 30  
Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Tyr Pro Gly Gln  
35 40 45  
Ala Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His  
50 55 60  
15 Gly Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro  
65 70 75 80  
Gly Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser  
85 90 95  
Ala Pro Gly Ala Tyr Pro Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly  
20 100 105 110  
Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro  
115 120 125  
Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg  
130 135 140

67/335

Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Asn  
145 150 155 160  
Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys  
165 170 175  
5 Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe  
180 185 190  
Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His  
195 200 205  
Phe Lys Val Ala Val Asn Asp Ala His Leu Leu Gln Tyr Asn His Arg  
10 210 215 220  
Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile  
225 230 235 240  
Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile  
245 250  
15  
  
<210> 18  
  
<211> 347  
  
<212> PRT  
20 <213> Homo sapiens  
  
<220>  
  
<221> Voltage-dependent anion-selective channel protein 2 (VDAC-2)  
  
<222> (1)..(347)  
  
<223> Accession No.as of 06 Dec 2002: P45880

68/335

&lt;400&gt; 18

Met Ser Trp Cys Asn Glu Leu Arg Leu Pro Ala Leu Lys Gln His Ser  
1 5 10 15  
5 Ile Gly Arg Gly Leu Glu Ser His Ile Thr Met Cys Ile Pro Pro Ser  
20 25 30  
Tyr Ala Asp Leu Gly Lys Ala Ala Arg Asp Ile Phe Asn Lys Gly Phe  
35 40 45  
Gly Phe Gly Leu Val Lys Leu Asp Val Lys Thr Lys Ser Cys Ser Gly  
10 50 55 60  
Val Glu Phe Ser Thr Ser Gly Ser Ser Asn Thr Asp Thr Gly Lys Val  
65 70 75 80  
Thr Gly Thr Leu Glu Thr Lys Tyr Lys Trp Cys Glu Tyr Gly Leu Thr  
85 90 95  
15 Phe Thr Glu Lys Trp Asn Thr Asp Asn Thr Leu Gly Thr Glu Ile Ala  
100 105 110  
Ile Glu Asp Gln Ile Cys Gln Gly Leu Lys Leu Thr Phe Asp Thr Thr  
115 120 125  
Phe Ser Pro Asn Thr Gly Lys Lys Ser Gly Lys Ile Lys Ser Ser Tyr  
20 130 135 140  
Lys Arg Glu Cys Ile Asn Leu Gly Cys Asp Val Asp Phe Asp Phe Ala  
145 150 155 160  
Gly Pro Ala Ile His Gly Ser Ala Val Phe Gly Tyr Glu Gly Trp Leu  
165 170 175

69/335

Ala Gly Tyr Gln Met Thr Phe Asp Ser Ala Lys Ser Lys Leu Thr Arg  
180 185 190  
Asn Asn Phe Ala Val Gly Tyr Arg Thr Gly Asp Phe Gln Leu His Thr  
195 200 205  
5 Asn Val Asn Asp Gly Thr Glu Phe Gly Gly Ser Ile Tyr Gln Lys Val  
210 215 220  
Cys Glu Asp Leu Asp Thr Ser Val Asn Leu Ala Trp Thr Ser Gly Thr  
225 230 235 240  
Asn Cys Thr Arg Phe Gly Ile Ala Ala Lys Tyr Gln Leu Asp Pro Thr  
10 245 250 255  
Ala Ser Ile Ser Ala Lys Val Asn Asn Ser Ser Leu Ile Gly Val Gly  
260 265 270  
Tyr Thr Gln Thr Leu Arg Pro Gly Val Lys Leu Thr Leu Ser Ala Leu  
275 280 285  
15 Val Asp Gly Lys Ser Ile Asn Ala Gly Gly His Lys Val Gly Ser Pro  
290 295 300  
Trp Ser Trp Arg Leu Asn Pro Ala Glu Arg Asn Leu Trp Glu Trp Ile  
305 310 315 320  
Ser Glu Asp Leu Ala Leu Ile Tyr Phe His Cys Asp Gln Gln Gln Ala  
20 325 330 335  
Phe Phe Pro Pro Glu Asp Asp Gln Asn Lys Gly  
340 345

70/335

&lt;210&gt; 19

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; Annexin II

&lt;222&gt; (1)..(339)

&lt;223&gt; Accession No. as of 06 Dec 2002: P07355

&lt;400&gt; 19

10

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp

1 5 10 15

His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn

20 25 30

15 Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser

50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys

20 65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu

85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser

100 105 110



Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu  
115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn  
130 135 140

5 Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile  
145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys  
165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp  
10 180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr  
195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His  
210 215 220

15 Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met  
225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe  
245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp  
20 260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu  
275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg  
290 295 300

72/335

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln

305 310 315 320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly

325 330 335

5 Gly Asp Asp

&lt;210&gt; 20

10 &lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Collagen-binding protein 2 precursor

15 &lt;222&gt; (1)..(418)

&lt;223&gt; Accession No. as of 06 Dec 2002: P50454

&lt;400&gt; 20

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala

20 1 5 10 15

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr

20 25 30

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala

35

40

45

Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val  
50 55 60  
Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu  
65 70 75 80  
5 Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val  
85 90 95  
Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly  
100 105 110  
Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp  
10 115 120 125  
Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp  
130 135 140  
Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys  
145 150 155 160  
15 Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp  
165 170 175  
Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val  
180 185 190  
Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro  
20 195 200 205  
His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe  
210 215 220  
Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr  
225 230 235 240

74/335

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val  
 245 250 255  
 Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro  
 260 265 270  
 5 His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu  
 275 280 285  
 Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile  
 290 295 300  
 Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His  
 10 305 310 315 320  
 Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp  
 325 330 335  
 Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe  
 340 345 350  
 15 His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln  
 355 360 365  
 Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala  
 370 375 380  
 Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu  
 20 385 390 395 400  
 Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp  
 405 410 415  
 Glu Leu

<210> 21  
<211> 166  
5 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Cofilin, non-muscle isoform  
<222> (1)..(166)  
10 <223> Accession No. as of 08 ec 2002: P23528  
<400> 21

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn  
1 5 10 15  
15 Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg  
20 25 30  
Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile  
35 40 45  
Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val  
20 50 55 60  
Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys  
65 70 75 80  
Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys  
85 90 95

76/335

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys  
100 105 110  
Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu  
115 120 125  
5 Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys  
130 135 140  
Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser  
145 150 155 160  
Leu Glu Gly Lys Pro Leu  
10 165

<210> 22  
<211> 165  
15 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Peptidyl-prolyl cis-trans isomerase A  
<222> (1)..(165)  
20 <223> Accession No. as of 09 Dec 2002: P05092  
<400> 22

Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro  
1 5 10 15

77/335

Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr  
20 25 30  
Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr  
35 40 45  
5 Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly  
50 55 60  
Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly  
65 70 75 80  
Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly  
10 85 90 95  
Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe  
100 105 110  
Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val  
115 120 125  
15 Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg  
130 135 140  
Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ile Ala Asp  
145 150 155 160  
Cys Gly Gln Leu Glu  
20 165

&lt;210&gt; 23

&lt;211&gt; 638

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Dynein intermediate chain 2, cytosolic

5 &lt;222&gt; (1)..(638)

&lt;223&gt; Accession No. as of 09 Dec 2002: Q13409

&lt;400&gt; 23

Met Ser Asp Lys Ser Glu Leu Lys Ala Glu Leu Glu Arg Lys Lys Gln  
10 1 5 10 15  
Arg Leu Ala Gln Ile Arg Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg  
20 25 30  
Lys Lys Lys Glu Thr Asp Gln Lys Lys Glu Ala Val Ala Pro Val Gln  
35 40 45  
15 Glu Glu Ser Asp Leu Glu Lys Lys Arg Arg Glu Ala Glu Ala Leu Leu  
50 55 60  
Gln Ser Met Gly Leu Thr Pro Glu Ser Pro Ile Val Phe Ser Glu Tyr  
65 70 75 80  
Trp Val Pro Pro Pro Met Ser Pro Ser Ser Lys Ser Val Ser Thr Pro  
20 85 90 95  
Ser Glu Ala Gly Ser Gln Asp Ser Gly Asp Gly Ala Val Gly Ser Arg  
100 105 110  
Thr Leu His Trp Asp Thr Asp Pro Ser Val Leu Gln Leu His Ser Asp  
115 120 125



Ser Asp Leu Gly Arg Gly Pro Ile Lys Leu Gly Met Ala Lys Ile Thr  
130 135 140  
Gln Val Asp Phe Pro Pro Arg Glu Ile Val Thr Tyr Thr Lys Glu Thr  
145 150 155 160  
5 Gln Thr Pro Val Met Ala Gln Pro Lys Glu Asp Glu Glu Glu Asp Asp  
165 170 175  
Asp Val Val Ala Pro Lys Pro Pro Ile Glu Pro Glu Glu Glu Lys Thr  
180 185 190  
Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro Pro His Glu Leu  
10 195 200 205  
Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu Glu Phe Leu Ser  
210 215 220  
Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala Leu Ser Glu Gln  
225 230 235 240  
15 Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu Glu Asp Lys Glu  
245 250 255  
Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn Arg Gln Phe Phe  
260 265 270  
Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys Leu Asp Trp Ser  
20 275 280 285  
Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn Asn Asn Glu Asp  
290 295 300  
Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp Asn Met Lys Tyr  
305 310 315 320

80/335

Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln Ser Ala Val Met  
325 330 335

Ser Ala Thr Phe Ala Lys Phe His Pro Asn Leu Val Val Gly Gly Thr  
340 345 350

5 Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser Asn Lys Arg Thr  
355 360 365

Pro Val Gln Arg Thr Pro Leu Ser Ala Ala Ala His Thr His Pro Val  
370 375 380

Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His Asn Leu Ile Ser  
10 385 390 395 400

Ile Ser Thr Asp Gly Lys Ile Cys Ser Trp Ser Leu Asp Met Leu Ser  
405 410 415

His Pro Gln Asp Ser Met Glu Leu Val His Lys Gln Ser Lys Ala Val  
420 425 430

15 Ala Val Thr Ser Met Ser Phe Pro Val Gly Asp Val Asn Asn Phe Val  
435 440 445

Val Gly Ser Glu Glu Gly Ser Val Tyr Thr Ala Cys Arg His Gly Ser  
450 455 460

Lys Ala Gly Ile Ser Glu Met Phe Glu Gly His Gln Gly Pro Ile Thr  
20 465 470 475 480

Gly Ile His Cys His Ala Ala Val Gly Ala Val Asp Phe Ser His Leu  
485 490 495

Phe Val Thr Ser Ser Phe Asp Trp Thr Val Lys Leu Trp Thr Thr Lys  
500 505 510

Asn Asn Lys Pro Leu Tyr Ser Phe Glu Asp Asn Ala Asp Tyr Val Tyr  
515 520 525  
Asp Val Met Trp Ser Pro Thr His Pro Ala Leu Phe Ala Cys Val Asp  
530 535 540  
5 Gly Met Gly Arg Leu Asp Leu Trp Asn Leu Asn Asn Asp Thr Glu Val  
545 550 555 560  
Pro Thr Ala Ser Ile Ser Val Glu Gly Asn Pro Ala Leu Asn Arg Val  
565 570 575  
Arg Trp Thr His Ser Gly Arg Glu Ile Ala Val Gly Asp Ser Glu Gly  
10 580 585 590  
Gln Ile Val Ile Tyr Asp Val Gly Glu Gln Ile Ala Val Pro Arg Asn  
595 600 605  
Asp Glu Trp Ala Arg Phe Gly Arg Thr Leu Ala Glu Ile Asn Ala Asn  
610 615 620  
15 Arg Ala Asp Ala Glu Glu Glu Ala Ala Thr Arg Ile Pro Ala  
625 630 635

<210> 24  
20 <211> 328  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor

&lt;222&gt; (1) .. (328)

&lt;223&gt; Accession No. as of 09 Dec 2002: Q13011

&lt;400&gt; 24

5 Met Ala Ala Gly Ile Val Ala Ser Arg Arg Leu Arg Asp Leu Leu Thr  
1 5 10 15  
Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg  
20 25 30  
Leu Thr Gly Ser Ser Ala Gln Glu Glu Ala Ser Gly Val Ala Leu Gly  
10 35 40 45  
Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln  
50 55 60  
Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala  
65 70 75 80  
15 Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile  
85 90 95  
Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys  
100 105 110  
Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu  
20 115 120 125  
Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp  
130 135 140  
Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro  
145 150 155 160

83/335

Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val  
165 170 175

Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe  
180 185 190

5 Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr  
195 200 205

Leu Glu Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val Asn Glu  
210 215 220

Leu Ala Phe Thr Ala His Lys Met Met Ala Asp Glu Ala Leu Asp Ser  
10 225 230 235 240

Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala  
245 250 255

Ala Leu Pro Leu Ala Pro Glu Ile Ser Ser Lys Thr Thr Val Leu Val  
260 265 270

15 Gln Ser Thr Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala  
275 280 285

Glu Ser Leu Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr  
290 295 300

Gln Asp Leu Val Lys Ser Val Gln Pro Thr Thr Glu Asn Lys Glu Leu  
20 305 310 315 320

Lys Thr Val Thr Phe Ser Lys Leu  
325

&lt;210&gt; 25

&lt;211&gt; 1657

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; Ras GTPase-activating-like protein IQGAP1

&lt;222&gt; (1)..(1657)

&lt;223&gt; Accession No. as of 09 Dec 2002: P46940

&lt;400&gt; 25

10

Met Ser Ala Ala Asp Glu Val Asp Gly Leu Gly Val Ala Arg Pro His

1 5 10 15

Tyr Gly Ser Val Leu Asp Asn Glu Arg Leu Thr Ala Glu Glu Met Asp

20 25 30

15 Glu Arg Arg Arg Gln Asn Val Ala Tyr Glu Tyr Leu Cys His Leu Glu

35 40 45

Glu Ala Lys Arg Trp Met Glu Ala Cys Leu Gly Glu Asp Leu Pro Pro

50 55 60

Thr Thr Glu Leu Glu Glu Gly Leu Arg Asn Gly Val Tyr Leu Ala Lys

20 65 70 75 80

Leu Gly Asn Phe Phe Ser Pro Lys Val Val Ser Leu Lys Lys Ile Tyr

85 90 95

Asp Arg Glu Gln Thr Arg Tyr Lys Ala Thr Gly Leu His Phe Arg His

100 105 110

Thr Asp Asn Val Ile Gln Trp Leu Asn Ala Met Asp Glu Ile Gly Leu  
115 120 125

Pro Lys Ile Phe Tyr Pro Glu Thr Thr Asp Ile Tyr Asp Arg Lys Asn  
130 135 140

5 Met Pro Arg Cys Ile Tyr Cys Ile His Ala Leu Ser Leu Tyr Leu Phe  
145 150 155 160

Lys Leu Gly Leu Ala Pro Gln Ile Gln Asp Leu Tyr Gly Lys Val Asp  
165 170 175

Phe Thr Glu Glu Glu Ile Asn Asn Met Lys Thr Glu Leu Glu Lys Tyr  
10 180 185 190

Gly Ile Gln Met Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn  
195 200 205

Glu Leu Ser Val Asp Glu Ala Ala Leu His Ala Ala Val Ile Ala Ile  
210 215 220

15 Asn Glu Ala Ile Asp Arg Arg Ile Pro Ala Asp Thr Phe Ala Ala Leu  
225 230 235 240

Lys Asn Pro Asn Ala Met Leu Val Asn Leu Glu Glu Pro Leu Ala Ser  
245 250 255

Thr Tyr Gln Asp Ile Leu Tyr Gln Ala Lys Gln Asp Lys Met Thr Asn  
20 260 265 270

Ala Lys Asn Arg Thr Glu Asn Ser Glu Arg Glu Arg Asp Val Tyr Glu  
275 280 285

Glu Leu Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn Lys Val Asn  
290 295 300

86/335

Thr Phe Ser Ala Leu Ala Asn Ile Asp Leu Ala Leu Glu Gln Gly Asp  
305 310 315 320  
Ala Leu Ala Leu Phe Arg Ala Leu Gln Ser Pro Ala Leu Gly Leu Arg  
325 330 335  
5 Gly Leu Gln Gln Gln Asn Ser Asp Trp Tyr Leu Lys Gln Leu Leu Ser  
340 345 350  
Asp Lys Gln Gln Lys Arg Gln Ser Gly Gln Thr Asp Pro Leu Gln Lys  
355 360 365  
Glu Glu Leu Gln Ser Gly Val Asp Ala Ala Asn Ser Ala Ala Gln Gln  
10 370 375 380  
Tyr Gln Arg Arg Leu Ala Ala Val Ala Leu Ile Asn Ala Ala Ile Gln  
385 390 395 400  
Lys Gly Val Ala Glu Lys Thr Val Leu Glu Leu Met Asn Pro Glu Ala  
405 410 415  
15 Gln Leu Pro Gln Val Tyr Pro Phe Ala Ala Asp Leu Tyr Gln Lys Glu  
420 425 430  
Leu Ala Thr Leu Gln Arg Gln Ser Pro Glu His Asn Leu Thr His Pro  
435 440 445  
Glu Leu Ser Val Ala Val Glu Met Leu Ser Ser Val Ala Leu Ile Asn  
20 450 455 460  
Arg Ala Leu Glu Ser Gly Asp Val Asn Thr Val Trp Lys Gln Leu Ser  
465 470 475 480  
Ser Ser Val Thr Gly Leu Thr Asn Ile Glu Glu Glu Asn Cys Gln Arg  
485 490 495



Tyr Leu Asp Glu Leu Met Lys Leu Lys Ala Gln Ala His Ala Glu Asn  
500 505 510  
Asn Glu Phe Ile Thr Trp Asn Asp Ile Gln Ala Cys Val Asp His Val  
515 520 525  
5 Asn Leu Val Val Gln Glu Glu His Glu Arg Ile Leu Ala Ile Gly Leu  
530 535 540  
Ile Asn Glu Ala Leu Asp Glu Gly Asp Ala Gln Lys Thr Leu Gln Ala  
545 550 555 560  
Leu Gln Ile Pro Ala Ala Lys Leu Glu Gly Val Leu Ala Glu Val Ala  
10 565 570 575  
Gln His Tyr Gln Asp Thr Leu Ile Arg Ala Lys Arg Glu Lys Ala Gln  
580 585 590  
Glu Ile Gln Asp Glu Ser Ala Val Leu Trp Leu Asp Glu Ile Gln Gly  
595 600 605  
15 Gly Ile Trp Gln Ser Asn Lys Asp Thr Gln Glu Ala Gln Lys Phe Ala  
610 615 620  
Leu Gly Ile Phe Ala Ile Asn Glu Ala Val Glu Ser Gly Asp Val Gly  
625 630 635 640  
Lys Thr Leu Ser Ala Leu Arg Ser Pro Asp Val Gly Leu Tyr Gly Val  
20 645 650 655  
Ile Pro Glu Cys Gly Glu Thr Tyr His Ser Asp Leu Ala Glu Ala Lys  
660 665 670  
Lys Lys Lys Leu Ala Val Gly Asp Asn Asn Ser Lys Trp Val Lys His  
675 680 685

88/335

Trp Val Lys Gly Gly Tyr Tyr Tyr Tyr His Asn Leu Glu Thr Gln Glu  
 690 695 700  
 Gly Gly Trp Asp Glu Pro Pro Asn Phe Val Gln Asn Ser Met Gln Leu  
 705 710 715 720  
 5 Ser Arg Glu Glu Ile Gln Ser Ser Ile Ser Gly Val Thr Ala Ala Tyr  
 725 730 735  
 Asn Arg Glu Gln Leu Trp Leu Ala Asn Glu Gly Leu Ile Thr Arg Leu  
 740 745 750  
 Gln Ala Arg Cys Arg Gly Tyr Leu Val Arg Gln Glu Phe Arg Ser Arg  
 10 755 760 765  
 Met Asn Phe Leu Lys Lys Gln Ile Pro Ala Ile Thr Cys Ile Gln Ser  
 770 775 780  
 Gln Trp Arg Gly Tyr Lys Gln Lys Lys Ala Tyr Gln Asp Arg Leu Ala  
 785 790 795 800  
 15 Tyr Leu Arg Ser His Lys Asp Glu Val Val Lys Ile Gln Ser Leu Ala  
 805 810 815  
 Arg Met His Gln Ala Arg Lys Arg Tyr Arg Asp Arg Leu Gln Tyr Phe  
 820 825 830  
 Arg Asp His Ile Asn Asp Ile Ile Lys Ile Gln Ala Phe Ile Arg Ala  
 20 835 840 845  
 Asn Lys Ala Arg Asp Asp Tyr Lys Thr Leu Ile Asn Ala Glu Asp Pro  
 850 855 860  
 Pro Met Val Val Val Arg Lys Phe Val His Leu Leu Asp Gln Ser Asp  
 865 870 875 880

Gln Asp Phe Gln Glu Glu Leu Asp Leu Met Lys Met Arg Glu Glu Val  
885 890 895

Ile Thr Leu Ile Arg Ser Asn Gln Gln Leu Glu Asn Asp Leu Asn Leu  
900 905 910

5 Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Lys Ile Thr Leu Gln  
915 920 925

Asp Val Val Ser His Ser Lys Lys Leu Thr Lys Lys Asn Lys Glu Gln  
930 935 940

Leu Ser Asp Met Met Met Ile Asn Lys Gln Lys Gly Gly Leu Lys Ala  
10 945 950 955 960

Leu Ser Lys Glu Lys Arg Glu Lys Leu Glu Ala Tyr Gln His Leu Phe  
965 970 975

Tyr Leu Leu Gln Thr Asn Pro Thr Tyr Leu Ala Lys Leu Ile Phe Gln  
980 985 990

15 Met Pro Gln Asn Lys Ser Thr Lys Phe Met Asp Ser Val Ile Phe Thr  
995 1000 1005

Leu Tyr Asn Tyr Ala Ser Asn Gln Arg Glu Glu Tyr Leu Leu Leu  
1010 1015 1020

Arg Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val  
20 1025 1030 1035

Asp Gln Ile Gln Glu Ile Val Thr Gly Asn Pro Thr Val Ile Lys  
1040 1045 1050

Met Val Val Ser Phe Asn Arg Gly Ala Arg Gly Gln Asn Ala Leu  
1055 1060 1065

90/335

	Arg	Gln	Ile	Leu	Ala	Pro	Val	Val	Lys	Glu	Ile	Met	Asp	Asp	Lys
	1070						1075					1080			
	Ser	Leu	Asn	Ile	Lys	Thr	Asp	Pro	Val	Asp	Ile	Tyr	Lys	Ser	Trp
	1085						1090					1095			
5	Val	Asn	Gln	Met	Glu	Ser	Gln	Thr	Gly	Glu	Ala	Ser	Lys	Leu	Pro
	1100						1105					1110			
	Tyr	Asp	Val	Thr	Pro	Glu	Gln	Ala	Leu	Ala	His	Glu	Glu	Val	Lys
	1115						1120					1125			
	Thr	Arg	Leu	Asp	Ser	Ser	Ile	Arg	Asn	Met	Arg	Ala	Val	Thr	Asp
10	1130						1135					1140			
	Lys	Phe	Leu	Ser	Ala	Ile	Val	Ser	Ser	Val	Asp	Lys	Ile	Pro	Tyr
	1145						1150					1155			
	Gly	Met	Arg	Phe	Ile	Ala	Lys	Val	Leu	Lys	Asp	Ser	Leu	His	Glu
	1160						1165					1170			
15	Lys	Phe	Pro	Asp	Ala	Gly	Glu	Asp	Glu	Leu	Leu	Lys	Ile	Ile	Gly
	1175						1180					1185			
	Asn	Leu	Leu	Tyr	Tyr	Arg	Tyr	Met	Asn	Pro	Ala	Ile	Val	Ala	Pro
	1190						1195					1200			
	Asp	Ala	Phe	Asp	Ile	Ile	Asp	Leu	Ser	Ala	Gly	Gly	Gln	Leu	Thr
20	1205						1210					1215			
	Thr	Asp	Gln	Arg	Arg	Asn	Leu	Gly	Ser	Ile	Ala	Lys	Met	Leu	Gln
	1220						1225					1230			
	His	Ala	Ala	Ser	Asn	Lys	Met	Phe	Leu	Gly	Asp	Asn	Ala	His	Leu
	1235						1240					1245			

	Ser Ile	Ile Asn Glu Tyr Leu	Ser Gln Ser Tyr Gln	Lys Phe Arg
	1250		1255	1260
	Arg Phe	Phe Gln Thr Ala Cys	Asp Val Pro Glu Leu	Gln Asp Lys
	1265		1270	1275
5	Phe Asn	Val Asp Glu Tyr Ser	Asp Leu Val Thr Leu	Thr Lys Pro
	1280		1285	1290
	Val Ile	Tyr Ile Ser Ile Gly	Glu Ile Ile Asn Thr	His Thr Leu
	1295		1300	1305
	Leu Leu	Asp His Gln Asp Ala	Ile Ala Pro Glu His	Asn Asp Pro
10	1310		1315	1320
	Ile His	Glu Leu Leu Asp Asp	Leu Gly Glu Val Pro	Thr Ile Glu
	1325		1330	1335
	Ser Leu	Ile Gly Glu Ser Ser	Gly Asn Leu Asn Asp	Pro Asn Lys
	1340		1345	1350
15	Glu Ala	Leu Ala Lys Thr Glu	Val Ser Leu Thr Leu	Thr Asn Lys
	1355		1360	1365
	Phe Asp	Val Pro Gly Asp Glu	Asn Ala Glu Met Asp	Ala Arg Thr
	1370		1375	1380
	Ile Leu	Leu Asn Thr Lys Arg	Leu Ile Val Asp Val	Ile Arg Phe
20	1385		1390	1395
	Gln Pro	Gly Glu Thr Leu Thr	Glu Ile Leu Glu Thr	Pro Ala Thr
	1400		1405	1410
	Ser Glu	Gln Glu Ala Glu His	Gln Arg Ala Met Gln	Arg Arg Ala
	1415		1420	1425

92/335

	Ile	Arg	Asp	Ala	Lys	Thr	Pro	Asp	Lys	Met	Lys	Lys	Ser	Lys	Ser
	1430						1435						1440		
	Val	Lys	Glu	Asp	Ser	Asn	Leu	Thr	Leu	Gln	Glu	Lys	Lys	Glu	Lys
	1445						1450						1455		
5	Ile	Gln	Thr	Gly	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Gly	Thr	Val	Asp
	1460						1465						1470		
	Pro	Lys	Asn	Lys	Tyr	Gln	Glu	Leu	Ile	Asn	Asp	Ile	Ala	Arg	Asp
	1475						1480						1485		
	Ile	Arg	Asn	Gln	Arg	Arg	Tyr	Arg	Gln	Arg	Arg	Lys	Ala	Glu	Leu
10	1490						1495						1500		
	Val	Lys	Leu	Gln	Gln	Thr	Tyr	Ala	Ala	Leu	Asn	Ser	Lys	Ala	Thr
	1505						1510						1515		
	Phe	Tyr	Gly	Glu	Gln	Val	Asp	Tyr	Tyr	Lys	Ser	Tyr	Ile	Lys	Thr
	1520						1525						1530		
15	Cys	Leu	Asp	Asn	Leu	Ala	Ser	Lys	Gly	Lys	Val	Ser	Lys	Lys	Pro
	1535						1540						1545		
	Arg	Glu	Met	Lys	Gly	Lys	Lys	Ser	Lys	Lys	Ile	Ser	Leu	Lys	Tyr
	1550						1555						1560		
	Thr	Ala	Ala	Arg	Leu	His	Glu	Lys	Gly	Val	Leu	Leu	Glu	Ile	Glu
20	1565						1570						1575		
	Asp	Leu	Gln	Val	Asn	Gln	Phe	Lys	Asn	Val	Ile	Phe	Glu	Ile	Ser
	1580						1585						1590		
	Pro	Thr	Glu	Glu	Val	Gly	Asp	Phe	Glu	Val	Lys	Ala	Lys	Phe	Met
	1595						1600						1605		

93/335

Gly Val Gln Met Glu Thr Phe Met Leu His Tyr Gln Asp Leu Leu

1610

1615

1620

Gln Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asp Arg

1625

1630

1635

5 Ala Lys Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys

1640

1645

1650

Phe Tyr Gly Lys

1655

10

&lt;210&gt; 26

&lt;211&gt; 627

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15 &lt;220&gt;

&lt;221&gt; L-plastin (Lymphocyte cytosolic protein 1)

&lt;222&gt; (1)..(627)

&lt;223&gt; Accession No. as of 09 Dec 2002: P13796

20 &lt;400&gt; 26

Met Ala Arg Gly Ser Val Ser Asp Glu Glu Met Met Glu Leu Arg Glu

1

5

10

15

Ala Phe Ala Lys Val Asp Thr Asp Gly Asn Gly Tyr Ile Ser Phe Asn

94/335

20 25 30  
 Glu Leu Asn Asp Leu Phe Lys Ala Ala Cys Leu Pro Leu Pro Gly Tyr  
 35 40 45  
 Arg Val Arg Glu Ile Thr Glu Asn Leu Met Ala Thr Gly Asp Leu Asp  
 5 50 55 60  
 Gln Asp Gly Arg Ile Ser Phe Asp Glu Phe Ile Lys Ile Phe His Gly  
 65 70 75 80  
 Leu Lys Ser Thr Asp Val Ala Lys Thr Phe Arg Lys Ala Ile Asn Lys  
 85 90 95  
 10 Lys Glu Gly Ile Cys Ala Ile Gly Gly Thr Ser Glu Gln Ser Ser Val  
 100 105 110  
 Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala Phe Val Asn  
 115 120 125  
 Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg His Val Ile  
 15 130 135 140  
 Pro Met Asn Pro Asn Thr Asn Asp Leu Phe Asn Ala Val Gly Asp Gly  
 145 150 155 160  
 Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp Thr Ile Asp  
 165 170 175  
 20 Glu Arg Thr Ile Asn Lys Lys Lys Leu Thr Pro Phe Thr Ile Gln Glu  
 180 185 190  
 Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly Cys His Val  
 195 200 205  
 Val Asn Ile Gly Ala Glu Asp Leu Lys Glu Gly Lys Pro Tyr Leu Val



95/335

210 215 220  
Leu Gly Leu Leu Trp Gln Val Ile Lys Ile Gly Leu Phe Ala Asp Ile  
225 230 235 240  
Glu Leu Ser Arg Asn Glu Ala Leu Ile Ala Leu Leu Arg Glu Gly Glu  
5 245 250 255  
Ser Leu Glu Asp Leu Met Lys Leu Ser Pro Glu Glu Leu Leu Leu Arg  
260 265 270  
Trp Ala Asn Tyr His Leu Glu Asn Ala Gly Cys Asn Lys Ile Gly Asn  
275 280 285  
10 Phe Ser Thr Asp Ile Lys Asp Ser Lys Ala Tyr Tyr His Leu Leu Glu  
290 295 300  
Gln Val Ala Pro Lys Gly Asp Glu Glu Gly Val Pro Ala Val Val Ile  
305 310 315 320  
Asp Met Ser Gly Leu Arg Glu Lys Asp Asp Ile Gln Arg Ala Glu Cys  
15 325 330 335  
Met Leu Gln Gln Ala Glu Arg Leu Gly Cys Arg Gln Phe Val Thr Ala  
340 345 350  
Thr Asp Val Val Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala  
355 360 365  
20 Asn Leu Phe Asn Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp  
370 375 380  
Ile Asp Trp Gly Ala Leu Glu Gly Glu Thr Arg Glu Glu Arg Thr Phe  
385 390 395 400  
Arg Asn Trp Met Asn Ser Leu Gly Val Asn Pro Arg Val Asn His Leu

96/335

405 410 415  
Tyr Ser Asp Leu Ser Asp Ala Leu Val Ile Phe Gln Leu Tyr Glu Lys  
420 425 430  
Ile Lys Val Pro Val Asp Trp Asn Arg Val Asn Lys Pro Pro Tyr Pro  
5 435 440 445  
Lys Leu Gly Gly Asn Met Lys Lys Leu Glu Asn Cys Asn Tyr Ala Val  
450 455 460  
Glu Leu Gly Lys Asn Gln Ala Lys Phe Ser Leu Val Gly Ile Gly Gly  
465 470 475 480  
10 Gln Asp Leu Asn Glu Gly Asn Arg Thr Leu Thr Leu Ala Leu Ile Trp  
485 490 495  
Gln Leu Met Arg Arg Tyr Thr Leu Asn Ile Leu Glu Glu Ile Gly Gly  
500 505 510  
Gly Gln Lys Val Asn Asp Asp Ile Ile Val Asn Trp Val Asn Glu Thr  
15 515 520 525  
Leu Arg Glu Ala Glu Lys Ser Ser Ser Ile Ser Ser Phe Lys Asp Pro  
530 535 540  
Lys Ile Ser Thr Ser Leu Pro Val Leu Asp Leu Ile Asp Ala Ile Gln  
545 550 555 560  
20 Pro Gly Ser Ile Asn Tyr Asp Leu Leu Lys Thr Glu Asn Leu Asn Asp  
565 570 575  
Asp Glu Lys Leu Asn Asn Ala Lys Tyr Ala Ile Ser Met Ala Arg Lys  
580 585 590  
Ile Gly Ala Arg Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Asn

97/335

595

600

605

Pro Lys Met Val Met Thr Val Phe Ala Cys Leu Met Gly Lys Gly Met

610

615

620

Lys Arg Val

5 625

&lt;210&gt; 27

&lt;211&gt; 216

10 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; GTP-binding nuclear protein RAN

&lt;222&gt; (1)..(216)

15 &lt;223&gt; Accession No. as of 09 Dec 2002: P17080

&lt;400&gt; 27

Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val

1

5

10

15

20 Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr

20

25

30

Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His

35

40

45

Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp

98/335

50 55 60  
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr  
65 70 75 80  
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val  
5 85 90 95  
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys  
100 105 110  
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp  
115 120 125  
10 Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu  
130 135 140  
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro  
145 150 155 160  
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe  
15 165 170 175  
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala  
180 185 190  
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala  
195 200 205  
20 Leu Pro Asp Glu Asp Asp Asp Leu  
210 215

&lt;210&gt; 28

<211> 463

<212> PRT

<213> Homo sapiens

<220>

5 <221> Heterogeneous nuclear ribonucleoprotein K

<222> (1)..(463)

<223> Accession No. as of 09 Dec 2002: Q07244

<400> 28

10 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn  
1 5 10 15  
Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala  
20 25 30  
Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu  
15 35 40 45  
Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn  
50 55 60  
Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp  
65 70 75 80  
20 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr  
85 90 95  
Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu  
100 105 110  
Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp

100/335

115 120 125  
Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp  
130 135 140  
Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile  
5 145 150 155 160  
Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr  
165 170 175  
Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val  
180 185 190  
10 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile  
195 200 205  
Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro  
210 215 220  
Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr  
15 225 230 235 240  
Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg  
245 250 255  
Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro  
260 265 270  
20 Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly  
275 280 285  
Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala  
290 295 300  
Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu

101/335

305                      310                      315                      320  
Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met  
                         325                      330                      335  
Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp  
5                      340                      345                      350  
Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly  
                         355                      360                      365  
Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly  
                         370                      375                      380  
10 Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly  
385                      390                      395                      400  
Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu  
                         405                      410                      415  
Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp  
15                      420                      425                      430  
Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln  
                         435                      440                      445  
Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe  
                         450                      455                      460  
20

&lt;210&gt; 29

&lt;211&gt; 172

&lt;212&gt; PRT

<213> Homo sapiens

<220>

<221> Translationally controlled tumor protein (TCTP)

<222> (1)..(172)

5 <223> Accession No. as of 09 Dec 2002: P13693

<400> 29

Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp  
1 5 10 15  
10 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu  
20 25 30  
Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile  
35 40 45  
Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser  
15 50 55 60  
Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu  
65 70 75 80  
Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met  
85 90 95  
20 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys  
100 105 110  
Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn  
115 120 125  
Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly



103/335

130 135 140  
Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met  
145 150 155 160  
Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys  
5 165 170

<210> 30  
<211> 284  
10 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Tropomyosin 1 alpha chain  
<222> (1)..(284)  
15 <223> Accession No. as of 06 Dec 2002: P09493  
<400> 30

Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu  
1 5 10 15  
20 Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala  
20 25 30  
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys  
35 40 45  
Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu



105/335

245 250 255  
Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu  
260 265 270  
Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile  
5 275 280

<210> 31  
<211> 482  
10 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Thymidine phosphorylase precursor  
<222> (1)..(482)  
15 <223> Accession No. as of 09 Dec 2002: P19971  
<400> 31

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly  
1 5 10 15  
20 Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu  
20 25 30  
Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg  
35 40 45  
Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly

106/335

50 55 60  
Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu  
65 70 75 80  
Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala  
5 85 90 95  
Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu  
100 105 110  
Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val  
115 120 125  
10 Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser  
130 135 140  
Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser  
145 150 155 160  
Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu  
15 165 170 175  
Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val  
180 185 190  
Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val  
195 200 205  
20 Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val  
210 215 220  
Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala  
225 230 235 240  
Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val

107/335

	245	250	255
	Gly Val Gly Ala Ser Leu Gly Leu Arg Val Ala Ala Ala Leu Thr Ala		
	260	265	270
	Met Asp Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu		
5	275	280	285
	Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Pro Asp Leu Arg Asp		
	290	295	300
	Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala		
	305	310	315
			320
10	Gly Thr Gln Ala Gln Gly Ala Ala Arg Val Ala Ala Ala Leu Asp Asp		
	325	330	335
	Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val		
	340	345	350
	Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg		
15	355	360	365
	Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Leu Ala Pro		
	370	375	380
	Ala Asp Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu Ala Leu Val		
	385	390	395
			400
20	Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu Pro Leu Arg		
	405	410	415
	Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln Arg Leu Arg		
	420	425	430
	Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro Ala Leu Ser		

108/335

435 440 445  
Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu Ser Asp Arg  
450 455 460  
Ala Pro Phe Ala Ala Pro Leu Pro Phe Ala Glu Leu Val Leu Pro Pro  
5 465 470 475 480  
Gln Gln

10 <210> 32  
<211> 488  
<212> PRT  
<213> Homo sapiens  
<220>  
15 <221> Cytosol aminopeptidase  
<222> (1)..(488)  
<223> Accession No. as of 09 Dec 2002: P28838  
<400> 32

20 Met Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp  
1 5 10 15  
Asp Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu  
20 25 30  
Ala Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys

109/335

35 40 45  
Ala Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser  
50 55 60  
Val Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln  
5 65 70 75 80  
Glu Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala  
85 90 95  
Gly Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp  
100 105 110  
10 Pro Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu  
115 120 125  
Tyr Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala  
130 135 140  
Lys Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu  
15 145 150 155 160  
Phe Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala  
165 170 175  
Asn Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu  
180 185 190  
20 Lys Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp  
195 200 205  
Ile Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser  
210 215 220  
Asp Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn

225	230	235	240
Ala Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp			
245	250	255	
Ser Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg			
5 260	265	270	
Ala Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala			
275	280	285	
Ala Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys			
290	295	300	
10 Glu Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg			
305	310	315	320
Ala Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly			
325	330	335	
Arg Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro			
5 340	345	350	
Lys Val Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala			
355	360	365	
Leu Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp			
370	375	380	
0 Asn Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg			
385	390	395	400
Met Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu			
405	410	415	
Ala Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr			



111/335

420 425 430  
Ala Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His  
435 440 445  
Leu Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu  
5 450 455 460  
Arg Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu  
465 470 475 480  
Leu Arg Phe Ser Gln Asp Asn Ala  
485

10

<210> 33  
<211> 400  
<212> PRT  
15 <213> Homo sapiens  
<220>  
<221> Keratin, type I cytoskeletal 19  
<222> (1)..(400)  
<223> Accession No. as of 09 Dec 2002 : P08727

20

&lt;400&gt; 33

Met Thr Ser Tyr Ser Tyr Arg Gln Ser Ser Ala Thr Ser Ser Phe Gly

1

5

10

15

112/335

Gly Leu Gly Gly Gly Ser Val Arg Phe Gly Pro Gly Val Ala Phe Arg  
20 25 30

Ala Pro Ser Ile His Gly Gly Ser Gly Gly Arg Gly Val Ser Val Ser  
35 40 45

5 Ser Ala Arg Phe Val Ser Ser Ser Ser Ser Gly Gly Tyr Gly Gly Gly  
50 55 60

Tyr Gly Gly Val Leu Thr Ala Ser Asp Gly Leu Leu Ala Gly Asn Glu  
65 70 75 80

Lys Leu Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp  
10 85 90 95

Lys Val Arg Ala Leu Glu Ala Ala Asn Gly Glu Leu Glu Val Lys Ile  
100 105 110

Arg Asp Trp Tyr Gln Lys Gln Gly Pro Gly Pro Ser Arg Asp Tyr Ser  
115 120 125

15 His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg Asp Lys Ile Leu Gly Ala  
130 135 140

Thr Ile Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu  
145 150 155 160

Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg  
20 165 170 175

Met Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu  
180 185 190

Leu Thr Leu Ala Arg Thr Asp Leu Glu Met Gln Ile Glu Gly Leu Lys  
195 200 205

113/335

Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu Glu Glu Ile Ser Thr  
210 215 220

Leu Arg Gly Gln Val Gly Gly Gln Val Ser Val Glu Val Asp Ser Ala  
225 230 235 240

5 Pro Gly Thr Asp Leu Ala Lys Ile Leu Ser Asp Met Arg Ser Gln Tyr  
245 250 255

Glu Val Met Ala Glu Gln Asn Arg Lys Asp Ala Glu Ala Trp Phe Thr  
260 265 270

Ser Arg Thr Glu Glu Leu Asn Arg Glu Val Ala Gly His Thr Glu Gln  
10 275 280 285

Leu Gln Met Ser Arg Ser Glu Val Thr Asp Leu Arg Arg Thr Leu Gln  
290 295 300

Gly Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ala Leu  
305 310 315 320

15 Glu Asp Thr Leu Ala Glu Thr Glu Ala Arg Phe Gly Ala Gln Leu Ala  
325 330 335

His Ile Gln Ala Leu Ile Ser Gly Ile Glu Ala Gln Leu Ala Asp Val  
340 345 350

Arg Ala Asp Ser Glu Arg Gln Asn Gln Glu Tyr Gln Arg Leu Met Asp  
20 355 360 365

Ile Lys Ser Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Ser Leu Leu  
370 375 380

Glu Gly Gln Glu Asp His Tyr Asn Asn Leu Ser Ala Ser Lys Val Leu  
385 390 395 400

<210> 34

<211> 325

5 <212> PRT

<213> Homo sapiens

<220>

<221> Alcohol dehydrogenase [NADP+]

<222> (1)..(325)

10 <223> Accession No. as of 09 Dec 2002: P14550

<400> 34

Met Ala Ala Ser Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu

1 5 10 15

15 Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala

20 25 30

Val Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala

35 40 45

Ile Tyr Gly Asn Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val

20 50 55 60

Gly Pro Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys

65 70 75 80

Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg

85 90 95

115/335

Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met  
100 105 110

His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn  
115 120 125

5 Ala Asp Gly Thr Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp  
130 135 140

Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly  
145 150 155 160

Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala  
10 165 170 175

Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala  
180 185 190

Gln Asn Glu Leu Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr  
195 200 205

15 Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp  
210 215 220

Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys  
225 230 235 240

Tyr Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg  
20 245 250 255

Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln  
260 265 270

Asn Ile Lys Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln  
275 280 285

116/335

Leu Asn Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr

290

295

300

Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro

305

310

315

320

5 Phe Asn Asp Pro Tyr

325

<210> 35

10 <211> 270

<212> PRT

<213> Homo sapiens

<220>

<221> Elastase IIIA precursor

15 <222> (1) .. (270)

<223> Accession No. as of 09 Dec 2002: P09093

<400> 35

Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser

20 1

5

10

15

Gly Tyr Gly Pro Pro Ser Ser His Ser Ser Ser Arg Val Val His Gly

20

25

30

Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr

35

40

45

117/335

Glu Lys Ser Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala  
 50 55 60  
 Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Arg Asp Leu Thr  
 65 70 75 80  
 5 Tyr Gln Val Val Leu Gly Glu Tyr Asn Leu Ala Val Lys Glu Gly Pro  
 85 90 95  
 Glu Gln Val Ile Pro Ile Asn Ser Glu Glu Leu Phe Val His Pro Leu  
 100 105 110  
 Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys  
 10 115 120 125  
 Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu  
 130 135 140  
 Pro Pro Ala Gly Asp Ile Leu Pro Asn Lys Thr Pro Cys Tyr Ile Thr  
 145 150 155 160  
 15 Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln  
 165 170 175  
 Gln Ala Arg Leu Pro Val Val Asp Tyr Lys His Cys Ser Arg Trp Asn  
 180 185 190  
 Trp Trp Gly Ser Thr Val Lys Lys Thr Met Val Cys Ala Gly Gly Tyr  
 20 195 200 205  
 Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro  
 210 215 220  
 Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser  
 225 230 235 240

118/335

Gly Phe Gly Cys Asn Phe Ile Trp Lys Pro Thr Val Phe Thr Arg Val

245

250

255

Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His

260

265

270

5

&lt;210&gt; 36

&lt;211&gt; 509

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Dihydrolipoamide dehydrogenase, mitochondrial precursor

&lt;222&gt; (1)..(509)

&lt;223&gt; Accession No. as of 09 Dec 2002: P09622

15 &lt;400&gt; 36

Met Gln Ser Trp Ser Arg Val Tyr Cys Ser Leu Ala Lys Arg Gly His

1

5

10

15

Phe Asn Arg Ile Ser His Gly Leu Gln Gly Leu Ser Ala Val Pro Leu

20

20

25

30

Arg Thr Tyr Ala Asp Gln Pro Ile Asp Ala Asp Val Thr Val Ile Gly

35

40

45

Ser Gly Pro Gly Gly Tyr Val Ala Ala Ile Lys Ala Ala Gln Leu Gly

50

55

60



119/335

Phe Lys Thr Val Cys Ile Glu Lys Asn Glu Thr Leu Gly Gly Thr Cys  
65 70 75 80  
Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Leu Asn Asn Ser His  
85 90 95  
5 Tyr Tyr His Met Ala His Gly Thr Asp Phe Ala Ser Arg Gly Ile Glu  
100 105 110  
Met Ser Glu Val Arg Leu Asn Leu Asp Lys Met Met Glu Gln Lys Ser  
115 120 125  
Thr Ala Val Lys Ala Leu Thr Gly Gly Ile Ala His Leu Phe Lys Gln  
10 130 135 140  
Asn Lys Val Val His Val Asn Gly Tyr Gly Lys Ile Thr Gly Lys Asn  
145 150 155 160  
Gln Val Thr Ala Thr Lys Ala Asp Gly Gly Thr Gln Val Ile Asp Thr  
165 170 175  
15 Lys Asn Ile Leu Ile Ala Thr Gly Ser Glu Val Thr Pro Phe Pro Gly  
180 185 190  
Ile Thr Ile Asp Glu Asp Thr Ile Val Ser Ser Thr Gly Ala Leu Ser  
195 200 205  
Leu Lys Lys Val Pro Glu Lys Met Val Val Ile Gly Ala Gly Val Ile  
20 210 215 220  
Gly Val Glu Leu Gly Ser Val Trp Gln Arg Leu Gly Ala Asp Val Thr  
225 230 235 240  
Ala Val Glu Phe Leu Gly His Val Gly Gly Val Gly Ile Asp Met Glu  
245 250 255

120/335

Ile Ser Lys Asn Phe Gln Arg Ile Leu Gln Lys Gln Gly Phe Lys Phe  
260 265 270

Lys Leu Asn Thr Lys Val Thr Gly Ala Thr Lys Lys Ser Asp Gly Lys  
275 280 285

5 Ile Asp Val Ser Ile Glu Ala Ala Ser Gly Gly Lys Ala Glu Val Ile  
290 295 300

Thr Cys Asp Val Leu Leu Val Cys Ile Gly Arg Arg Pro Phe Thr Lys  
305 310 315 320

Asn Leu Gly Leu Glu Glu Leu Gly Ile Glu Leu Asp Pro Arg Gly Arg  
10 325 330 335

Ile Pro Val Asn Thr Arg Phe Gln Thr Lys Ile Pro Asn Ile Tyr Ala  
340 345 350

Ile Gly Asp Val Val Ala Gly Pro Met Leu Ala His Lys Ala Glu Asp  
355 360 365

15 Glu Gly Ile Ile Cys Val Glu Gly Met Ala Gly Gly Ala Val His Ile  
370 375 380

Asp Tyr Asn Cys Val Pro Ser Val Ile Tyr Thr His Pro Glu Val Ala  
385 390 395 400

Trp Val Gly Lys Ser Glu Glu Gln Leu Lys Glu Glu Gly Ile Glu Tyr  
20 405 410 415

Lys Val Gly Lys Phe Pro Phe Ala Ala Asn Ser Arg Ala Lys Thr Asn  
420 425 430

Ala Asp Thr Asp Gly Met Val Lys Ile Leu Gly Gln Lys Ser Thr Asp  
435 440 445

121/335

Arg Val Leu Gly Ala His Ile Leu Gly Pro Gly Ala Gly Glu Met Val  
450 455 460  
Asn Glu Ala Ala Leu Ala Leu Glu Tyr Gly Ala Ser Cys Glu Asp Ile  
465 470 475 480  
5 Ala Arg Val Cys His Ala His Pro Thr Leu Ser Glu Ala Phe Arg Glu  
485 490 495  
Ala Asn Leu Ala Ala Ser Phe Gly Lys Ser Ile Asn Phe  
500 505

10

&lt;210&gt; 37

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15 &lt;220&gt;

&lt;221&gt; Enoyl-CoA hydratase, mitochondrial precursor

&lt;222&gt; (1)..(290)

&lt;223&gt; Accession No. as of 09 Dec 2002: P30084

&lt;400&gt; 37

20

Met Ala Ala Leu Arg Val Leu Leu Ser Cys Ala Arg Gly Pro Leu Arg

1

5

10

15

Pro Pro Val Arg Cys Pro Ala Trp Arg Pro Phe Ala Ser Gly Ala Asn

20

25

30

122/335

Phe Glu Tyr Ile Ile Ala Glu Lys Arg Gly Lys Asn Asn Thr Val Gly  
35 40 45

Leu Ile Gln Leu Asn Arg Pro Lys Ala Leu Asn Ala Leu Cys Asp Gly  
50 55 60

5 Leu Ile Asp Glu Leu Asn Gln Ala Leu Lys Ile Phe Glu Glu Asp Pro  
65 70 75 80

Ala Val Gly Ala Ile Val Leu Thr Gly Gly Asp Lys Ala Phe Ala Ala  
85 90 95

Gly Ala Asp Ile Lys Glu Met Gln Asn Leu Ser Phe Gln Asp Cys Tyr  
10 100 105 110

Ser Ser Lys Phe Leu Lys His Trp Asp His Leu Thr Gln Val Lys Lys  
115 120 125

Pro Val Ile Ala Ala Val Asn Gly Tyr Ala Phe Gly Gly Gly Cys Glu  
130 135 140

15 Leu Ala Met Met Cys Asp Ile Ile Tyr Ala Gly Glu Lys Ala Gln Phe  
145 150 155 160

Ala Gln Pro Glu Ile Leu Ile Gly Thr Ile Pro Gly Ala Gly Gly Thr  
165 170 175

Gln Arg Leu Thr Arg Ala Val Gly Lys Ser Leu Ala Met Glu Met Val  
20 180 185 190

Leu Thr Gly Asp Arg Ile Ser Ala Gln Asp Ala Lys Gln Ala Gly Leu  
195 200 205

Val Ser Lys Ile Cys Pro Val Glu Thr Leu Val Glu Glu Ala Ile Gln  
210 215 220

123/335

Cys Ala Glu Lys Ile Ala Ser Asn Ser Lys Ile Val Val Ala Met Ala  
225 230 235 240  
Lys Glu Ser Val Asn Ala Ala Phe Glu Met Thr Leu Thr Glu Gly Ser  
245 250 255  
5 Lys Leu Glu Lys Lys Leu Phe Tyr Ser Thr Phe Ala Thr Asp Asp Arg  
260 265 270  
Lys Glu Gly Met Thr Ala Phe Val Glu Lys Arg Lys Ala Asn Phe Lys  
275 280 285  
Asp Gln  
10 290

<210> 38  
<211> 160  
15 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Heat-shock 20 kDa like-protein p20  
<222> (1)..(160)  
20 <223> Accession No. as of 09 Dec 2002: O14558  
<400> 38

Met Glu Ile Pro Val Pro Val Gln Pro Ser Trp Leu Arg Arg Ala Ser

1

5

10

15

124/335

Ala Pro Leu Pro Gly Leu Ser Ala Pro Gly Arg Leu Phe Asp Gln Arg  
20 25 30  
Phe Gly Glu Gly Leu Leu Glu Ala Glu Leu Ala Ala Leu Cys Pro Thr  
35 40 45  
5 Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val  
50 55 60  
Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val  
65 70 75 80  
Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His  
10 85 90 95  
Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe  
100 105 110  
Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp  
115 120 125  
15 Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile  
130 135 140  
Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Pro Ala Ala Ala Lys  
145 150 155 160

20

&lt;210&gt; 39

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

125/335

&lt;220&gt;

&lt;221&gt; Myosin light chain alkali, non-muscle isoform

&lt;222&gt; (1)..(151)

&lt;223&gt; Accession No. as of 09 Dec 2002: P16475

5 &lt;400&gt; 39

Met Cys Asp Phe Thr Glu Asp Gln Thr Ala Glu Phe Lys Glu Ala Phe  
1 5 10 15  
Gln Leu Phe Asp Arg Thr Gly Asp Gly Lys Ile Leu Tyr Ser Gln Cys  
10 20 25 30  
Gly Asp Val Met Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val  
35 40 45  
Leu Lys Val Leu Gly Asn Pro Lys Ser Asp Glu Met Asn Val Lys Val  
50 55 60  
15 Leu Asp Phe Glu His Phe Leu Pro Met Leu Gln Thr Val Ala Lys Asn  
65 70 75 80  
Lys Asp Gln Gly Thr Tyr Glu Asp Tyr Val Glu Gly Leu Arg Val Phe  
85 90 95  
Asp Lys Glu Gly Asn Gly Thr Val Met Gly Ala Glu Ile Arg His Val  
20 100 105 110  
Leu Val Thr Leu Gly Glu Lys Met Thr Glu Glu Glu Val Glu Met Leu  
115 120 125  
Val Ala Gly His Glu Asp Ser Asn Gly Cys Ile Asn Tyr Glu Ala Phe  
130 135 140

Val Arg His Ile Leu Ser Gly

145

150

5 <210> 40

<211> 592

<212> PRT

<213> Homo sapiens

<220>

10 <221> Calnexin precursor

<222> (1)..(592)

<223> Accession No. as of 09 Dec 2002: P27824

<400> 40

15 Met Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala

1

5

10

15

Ile Val Glu Ala His Asp Gly His Asp Asp Asp Val Ile Asp Ile Glu

20

25

30

Asp Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp

20

35

40

45

Thr Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val

50

55

60

Pro Thr Gly Glu Val Tyr Phe Ala Asp Ser Phe Asp Arg Gly Thr Leu

65

70

75

80



127/335

Ser Gly Trp Ile Leu Ser Lys Ala Lys Lys Asp Asp Thr Asp Asp Glu  
85 90 95

Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser  
100 105 110

5 Lys Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His  
115 120 125

His Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys  
130 135 140

Pro Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys  
10 145 150 155 160

Gly Gly Ala Tyr Val Lys Leu Leu Ser Lys Thr Pro Glu Leu Asn Leu  
165 170 175

Asp Gln Phe His Asp Lys Thr Pro Tyr Thr Ile Met Phe Gly Pro Asp  
180 185 190

15 Lys Cys Gly Glu Asp Tyr Lys Leu His Phe Ile Phe Arg His Lys Asn  
195 200 205

Pro Lys Thr Gly Ile Tyr Glu Glu Lys His Ala Lys Arg Pro Asp Ala  
210 215 220

Asp Leu Lys Thr Tyr Phe Thr Asp Lys Lys Thr His Leu Tyr Thr Leu  
20 225 230 235 240

Ile Leu Asn Pro Asp Asn Ser Phe Glu Ile Leu Val Asp Gln Ser Val  
245 250 255

Val Asn Ser Gly Asn Leu Leu Asn Asp Met Thr Pro Pro Val Asn Pro  
260 265 270

128/335

Ser Arg Glu Ile Glu Asp Pro Glu Asp Arg Lys Pro Glu Asp Trp Asp  
275 280 285

Glu Arg Pro Lys Ile Pro Asp Pro Glu Ala Val Lys Pro Asp Asp Trp  
290 295 300

5 Asp Glu Asp Ala Pro Ala Lys Ile Pro Asp Glu Glu Ala Thr Lys Pro  
305 310 315 320

Glu Gly Trp Leu Asp Asp Glu Pro Glu Tyr Val Pro Asp Pro Asp Ala  
325 330 335

Glu Lys Pro Glu Asp Trp Asp Glu Asp Met Asp Gly Glu Trp Glu Ala  
10 340 345 350

Pro Gln Ile Ala Asn Pro Arg Cys Glu Ser Ala Pro Gly Cys Gly Val  
355 360 365

Trp Gln Arg Pro Val Ile Asp Asn Pro Asn Tyr Lys Gly Lys Trp Lys  
370 375 380

15 Pro Pro Met Ile Asp Asn Pro Ser Tyr Gln Gly Ile Trp Lys Pro Arg  
385 390 395 400

Lys Ile Pro Asn Pro Asp Phe Phe Glu Asp Leu Glu Pro Phe Arg Met  
405 410 415

Thr Pro Phe Ser Ala Ile Gly Leu Glu Leu Trp Ser Met Thr Ser Asp  
20 420 425 430

Ile Phe Phe Asp Asn Phe Ile Ile Cys Ala Asp Arg Arg Ile Val Asp  
435 440 445

Asp Trp Ala Asn Asp Gly Trp Gly Leu Lys Lys Ala Ala Asp Gly Ala  
450 455 460

129/335

Ala Glu Pro Gly Val Val Gly Gln Met Ile Glu Ala Ala Glu Glu Arg  
465 470 475 480  
Pro Trp Leu Trp Val Val Tyr Ile Leu Thr Val Ala Leu Pro Val Phe  
485 490 495  
5 Leu Val Ile Leu Phe Cys Cys Ser Gly Lys Lys Gln Thr Ser Gly Met  
500 505 510  
Glu Tyr Lys Lys Thr Asp Ala Pro Gln Pro Asp Val Lys Glu Glu Glu  
515 520 525  
Glu Glu Lys Glu Glu Glu Lys Asp Lys Gly Asp Glu Glu Glu Glu Gly  
10 530 535 540  
Glu Glu Lys Leu Glu Glu Lys Gln Lys Ser Asp Ala Glu Glu Asp Gly  
545 550 555 560  
Gly Thr Val Ser Gln Glu Glu Glu Asp Arg Lys Pro Lys Ala Glu Glu  
565 570 575  
15 Asp Glu Ile Leu Asn Arg Ser Pro Arg Asn Arg Lys Pro Arg Arg Glu  
580 585 590

&lt;210&gt; 41

20 &lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Complement component 1

&lt;222&gt; (1)..(282)

&lt;223&gt; Accession No. as of 09 Dec 2002: Q07021

&lt;400&gt; 41

5 Met Leu Pro Leu Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val  
1 5 10 15  
Ala Gly Leu Arg Ala Ala Ala Pro Ala Ser Pro Phe Arg Gln Leu Leu  
20 25 30  
Gln Pro Ala Pro Arg Leu Cys Thr Arg Pro Phe Gly Leu Leu Ser Val  
10 35 40 45  
Arg Ala Gly Ser Glu Arg Arg Pro Gly Leu Leu Arg Pro Arg Gly Pro  
50 55 60  
Cys Ala Cys Gly Cys Gly Cys Gly Ser Leu His Thr Asp Gly Asp Lys  
65 70 75 80  
15 Ala Phe Val Asp Phe Leu Ser Asp Glu Ile Lys Glu Glu Arg Lys Ile  
85 90 95  
Gln Lys His Lys Thr Leu Pro Lys Met Ser Gly Gly Trp Glu Leu Glu  
100 105 110  
Leu Asn Gly Thr Glu Ala Lys Leu Val Arg Lys Val Ala Gly Glu Lys  
20 115 120 125  
Ile Thr Val Thr Phe Asn Ile Asn Asn Ser Ile Pro Pro Thr Phe Asp  
130 135 140  
Gly Glu Glu Glu Pro Ser Gln Gly Gln Lys Val Glu Glu Gln Glu Pro  
145 150 155 160

131/335

Glu Leu Thr Ser Thr Pro Asn Phe Val Val Glu Val Ile Lys Asn Asp  
165 170 175  
Asp Gly Lys Lys Ala Leu Val Leu Asp Cys His Tyr Pro Glu Asp Glu  
180 185 190  
5 Val Gly Gln Glu Asp Glu Ala Glu Ser Asp Ile Phe Ser Ile Arg Glu  
195 200 205  
Val Ser Phe Gln Ser Thr Gly Glu Ser Glu Trp Lys Asp Thr Asn Tyr  
210 215 220  
Thr Leu Asn Thr Asp Ser Leu Asp Trp Ala Leu Tyr Asp His Leu Met  
10 225 230 235 240  
Asp Phe Leu Ala Asp Arg Gly Val Asp Asn Thr Phe Ala Asp Glu Leu  
245 250 255  
Val Glu Leu Ser Thr Ala Leu Glu His Gln Glu Tyr Ile Thr Phe Leu  
260 265 270  
15 Glu Asp Leu Lys Ser Phe Val Lys Ser Gln  
275 280

<210> 42  
20 <211> 727  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

precursor

&lt;222&gt; (1)..(727)

&lt;223&gt; Accession No. as of 09 Dec 2002: P28331

&lt;400&gt; 42

5

Met Leu Arg Ile Pro Val Arg Arg Ala Leu Val Gly Leu Ser Lys Ser  
1 5 10 15  
Pro Lys Gly Cys Val Arg Thr Thr Ala Thr Ala Ala Ser Asn Leu Ile  
20 25 30  
10 Glu Val Phe Val Asp Gly Gln Ser Val Met Val Glu Pro Gly Thr Thr  
35 40 45  
Val Leu Gln Ala Cys Glu Lys Val Gly Met Gln Ile Pro Arg Phe Cys  
50 55 60  
Tyr His Glu Arg Leu Ser Val Ala Gly Asn Cys Arg Met Cys Leu Val  
15 65 70 75 80  
Glu Ile Glu Lys Ala Pro Lys Val Val Ala Ala Cys Ala Met Pro Val  
85 90 95  
Met Lys Gly Trp Asn Ile Leu Thr Asn Ser Glu Lys Ser Lys Lys Ala  
100 105 110  
20 Arg Glu Gly Val Met Glu Phe Leu Leu Ala Asn His Pro Leu Asp Cys  
115 120 125  
Pro Ile Cys Asp Gln Gly Gly Glu Cys Asp Leu Gln Asp Gln Ser Met  
130 135 140  
Met Phe Gly Asn Asp Arg Ser Arg Phe Leu Glu Gly Lys Arg Ala Val



134/335

340 345 350  
Ala Leu Lys Asp Leu Leu Asn Arg Val Asp Ser Asp Thr Leu Cys Thr  
355 360 365  
Glu Glu Val Phe Pro Thr Ala Gly Ala Gly Thr Asp Leu Arg Ser Asn  
5 370 375 380  
Tyr Leu Leu Asn Thr Thr Ile Ala Gly Val Glu Glu Ala Asp Val Val  
385 390 395 400  
Leu Leu Val Gly Thr Asn Pro Arg Phe Glu Ala Pro Leu Phe Asn Ala  
405 410 415  
10 Trp Ile Arg Lys Ser Trp Leu His Asn Asp Leu Lys Val Ala Leu Ile  
420 425 430  
Gly Ser Pro Val Asp Leu Thr Tyr Thr Tyr Asp His Leu Gly Asp Ser  
435 440 445  
Pro Lys Ile Leu Gln Asp Ile Ala Ser Gly Ser His Pro Phe Ser Gln  
15 450 455 460  
Val Leu Lys Glu Ala Lys Lys Pro Met Val Val Leu Gly Ser Ser Ala  
465 470 475 480  
Leu Gln Arg Asn Asp Gly Ala Ala Ile Leu Ala Ala Val Ser Ser Ile  
485 490 495  
20 Ala Gln Lys Ile Arg Met Thr Ser Gly Val Thr Gly Asp Trp Lys Val  
500 505 510  
Met Asn Ile Leu His Arg Ile Ala Ser Gln Val Ala Ala Leu Asp Leu  
515 520 525  
Gly Tyr Lys Pro Gly Val Glu Ala Ile Arg Lys Asn Pro Pro Lys Val



135/335

530 535 540  
Leu Phe Leu Leu Gly Ala Asp Gly Gly Cys Ile Thr Arg Gln Asp Leu  
545 550 555 560  
Pro Lys Asp Cys Phe Ile Ile Tyr Gln Gly His His Gly Asp Val Gly  
5 565 570 575  
Ala Pro Ile Ala Asp Val Ile Leu Pro Gly Ala Ala Tyr Thr Glu Lys  
580 585 590  
Ser Ala Thr Tyr Val Asn Thr Glu Gly Arg Ala Gln Gln Thr Lys Val  
595 600 605  
10 Ala Val Thr Pro Pro Gly Leu Ala Arg Glu Asp Trp Lys Ile Ile Arg  
610 615 620  
Ala Leu Ser Glu Ile Ala Gly Met Thr Leu Pro Tyr Asp Thr Leu Asp  
625 630 635 640  
Gln Val Arg Asn Arg Leu Glu Glu Phe Ser Pro Asn Leu Val Arg Tyr  
15 645 650 655  
Asp Asp Ile Glu Gly Ala Asn Tyr Phe Gln Gln Ala Asn Glu Leu Ser  
660 665 670  
Lys Leu Val Asn Gln Gln Leu Leu Ala Asp Pro Leu Val Pro Pro Gln  
675 680 685  
20 Leu Thr Leu Lys Asp Phe Tyr Met Thr Asp Ser Ile Ser Arg Ala Ser  
690 695 700  
Gln Thr Met Ala Lys Cys Val Lys Ala Val Thr Glu Gly Ala Gln Ala  
705 710 715 720  
Val Glu Glu Pro Ser Ile Cys

725

&lt;210&gt; 43

5 &lt;211&gt; 491

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Pre-B cell enhancing factor precursor

10 &lt;222&gt; (1)..(491)

&lt;223&gt; Accession No. as of 09 Dec 2002: P43490

&lt;400&gt; 43

Met Asn Pro Ala Ala Glu Ala Glu Phe Asn Ile Leu Leu Ala Thr Asp

15 1 5 10 15

Ser Tyr Lys Val Thr His Tyr Lys Gln Tyr Pro Pro Asn Thr Ser Lys

20 25 30

Val Tyr Ser Tyr Phe Glu Cys Arg Glu Lys Lys Thr Glu Asn Ser Lys

35 40 45

20 Leu Arg Lys Val Lys Tyr Glu Glu Thr Val Phe Tyr Gly Leu Gln Tyr

50 55 60

Ile Leu Asn Lys Tyr Leu Lys Gly Lys Val Val Thr Lys Glu Lys Ile

65 70 75 80

Gln Glu Ala Lys Asp Val Tyr Lys Glu His Phe Gln Asp Asp Val Phe

137/335

85 90 95  
Asn Glu Lys Gly Trp Asn Tyr Ile Leu Glu Lys Tyr Asp Gly His Leu  
100 105 110  
Pro Ile Glu Ile Lys Ala Val Pro Glu Gly Phe Val Ile Pro Arg Gly  
5 115 120 125  
Asn Val Leu Phe Thr Val Glu Asn Thr Asp Pro Glu Cys Tyr Trp Leu  
130 135 140  
Thr Asn Trp Ile Glu Thr Ile Leu Val Gln Ser Trp Tyr Pro Ile Thr  
145 150 155 160  
10 Val Ala Thr Asn Ser Arg Glu Gln Lys Lys Ile Leu Ala Lys Tyr Leu  
165 170 175  
Leu Glu Thr Ser Gly Asn Leu Asp Gly Leu Glu Tyr Lys Leu His Asp  
180 185 190  
Phe Gly Tyr Arg Gly Val Ser Ser Gln Glu Thr Ala Gly Ile Gly Ala  
15 195 200 205  
Ser Ala His Leu Val Asn Phe Lys Gly Thr Asp Thr Val Ala Gly Leu  
210 215 220  
Ala Leu Ile Lys Lys Tyr Tyr Gly Thr Lys Asp Pro Val Pro Gly Tyr  
225 230 235 240  
20 Ser Val Pro Ala Ala Glu His Ser Thr Ile Thr Ala Trp Gly Lys Asp  
245 250 255  
His Glu Lys Asp Ala Phe Glu His Ile Val Thr Gln Phe Ser Ser Val  
260 265 270  
Pro Val Ser Val Val Ser Asp Ser Tyr Asp Ile Tyr Asn Ala Cys Glu

138/335

275                                      280                                      285  
 Lys Ile Trp Gly Glu Asp Leu Arg His Leu Ile Val Ser Arg Ser Thr  
 290                                      295                                      300  
 Gln Ala Pro Leu Ile Ile Arg Pro Asp Ser Gly Asn Pro Leu Asp Thr  
 5 305                                      310                                      315                                      320  
 Val Leu Lys Val Leu Glu Ile Leu Gly Lys Lys Phe Pro Val Thr Glu  
 325                                      330                                      335  
 Asn Ser Lys Gly Tyr Lys Leu Leu Pro Pro Tyr Leu Arg Val Ile Gln  
 340                                      345                                      350  
 10 Gly Asp Gly Val Asp Ile Asn Thr Leu Gln Glu Ile Val Glu Gly Met  
 355                                      360                                      365  
 Lys Gln Lys Met Trp Ser Ile Glu Asn Ile Ala Phe Gly Ser Gly Gly  
 370                                      375                                      380  
 Gly Leu Leu Gln Lys Leu Thr Arg Asp Leu Leu Asn Cys Ser Phe Lys  
 15 385                                      390                                      395                                      400  
 Cys Ser Tyr Val Val Thr Asn Gly Leu Gly Ile Asn Val Phe Lys Asp  
 405                                      410                                      415  
 Pro Val Ala Asp Pro Asn Lys Arg Ser Lys Lys Gly Arg Leu Ser Leu  
 420                                      425                                      430  
 20 His Arg Thr Pro Ala Gly Asn Phe Val Thr Leu Glu Glu Gly Lys Gly  
 435                                      440                                      445  
 Asp Leu Glu Glu Tyr Gly Gln Asp Leu Leu His Thr Val Phe Lys Asn  
 450                                      455                                      460  
 Gly Lys Val Thr Lys Ser Tyr Ser Phe Asp Glu Ile Arg Lys Asn Ala

465                      470                      475                      480

Gln Leu Asn Ile Glu Leu Glu Ala Ala His His

                        485                      490

<210>	44
<211>	135
<212>	PRT
<213>	Homo sapiens

```
10  <220>

    <221>  Retinol-binding protein I, cellular

    <222>  (1)..(135)

    <223>  Accession No. as of 09 Dec 2002: P09455

    <400>  44
```

Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn

**1**                      **5**                      **10**                      **15**

Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys

20                          25                          30

20 Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp

35                      40                      45

His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp

50                      55                      60

Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp

65	70	75	80
Arg	Lys	Cys	Met
Thr	Thr	Val	Ser
Trp	Asp	Gly	Asp
Lys	Leu	Gln	Cys

Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu

5                                    100                                    105                                    110

Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys

115                      120                      125

Gln Val Phe Lys Lys Val Gln

130 135

<210> 45

<211> 544

<212> PRT

15 <213> Homo sapiens

**<220>**

<221> T-complex protein 1, gamma subunit

<222> (1) .. (544)

<223> Accession No. as of 09 Dec 2002: P49368

20      <400>      45

Met Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu

**1                      5                      10                      15**

Ser Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile

141/335

20 25 30  
Ala Asp Ile Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met  
35 40 45  
Leu Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala  
5 50 55 60  
Ile Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile  
65 70 75 80  
Glu Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser  
85 90 95  
10 Val Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu  
100 105 110  
Glu Gln Gln Met His Pro Thr Val Val Ile Ser Ala Tyr Arg Lys Ala  
115 120 125  
Leu Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp  
15 130 135 140  
Ile Ser Asp Ser Asp Met Met Leu Asn Ile Ile Asn Ser Ser Ile Thr  
145 150 155 160  
Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu  
165 170 175  
20 Asp Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile  
180 185 190  
Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile  
195 200 205  
Glu Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr

142/335

210 215 220  
His Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu  
225 230 235 240  
Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu  
5 245 250 255  
Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu  
260 265 270  
Tyr Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val  
275 280 285  
10 Val Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met  
290 295 300  
Arg Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn  
305 310 315 320  
Arg Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu  
15 325 330 335  
Leu Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys  
340 345 350  
Lys Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro  
355 360 365  
20 Lys Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser  
370 375 380  
Glu Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val  
385 390 395 400  
Leu Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala



143/335

405 410 415  
Val Ala His Ala Leu Thr Glu Lys Ser Lys Ala Met Thr Gly Val Glu  
420 425 430  
Gln Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg  
5 435 440 445  
Thr Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser  
450 455 460  
Leu Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn  
465 470 475 480  
10 Gly Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu  
485 490 495  
Pro Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala  
500 505 510  
Val Leu Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys  
15 515 520 525  
Gly Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu  
530 535 540

20 &lt;210&gt; 46

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

144/335

&lt;221&gt; Placental ribonuclease inhibitor

&lt;222&gt; (1)..(461)

&lt;223&gt; Accession No. as of 09 Dec 2002: P13489

&lt;400&gt; 46

5

Met Ser Leu Asp Ile Gln Ser Leu Asp Ile Gln Cys Glu Glu Leu Ser

1 5 10 15

Asp Ala Arg Trp Ala Glu Leu Leu Pro Leu Leu Gln Gln Cys Gln Val

20 25 30

10 Val Arg Leu Asp Asp Cys Gly Leu Thr Glu Ala Arg Cys Lys Asp Ile

35 40 45

Ser Ser Ala Leu Arg Val Asn Pro Ala Leu Ala Glu Leu Asn Leu Arg

50 55 60

Ser Asn Glu Leu Gly Asp Val Gly Val His Cys Val Leu Gln Gly Leu

15 65 70 75 80

Gln Thr Pro Ser Cys Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Cys

85 90 95

Leu Thr Gly Ala Gly Cys Gly Val Leu Ser Ser Thr Leu Arg Thr Leu

100 105 110

20 Pro Thr Leu Gln Glu Leu His Leu Ser Asp Asn Leu Leu Gly Asp Ala

115 120 125

Gly Leu Gln Leu Leu Cys Glu Gly Leu Leu Asp Pro Gln Cys Arg Leu

130 135 140

Glu Lys Leu Gln Leu Glu Tyr Cys Ser Leu Ser Ala Ala Ser Cys Glu

	145	150	155	160												
	Pro	Leu	Ala	Ser	Val	Leu	Arg	Ala	Lys	Pro	Asp	Phe	Lys	Glu	Leu	Thr
		165		170		175										
	Val	Ser	Asn	Asn	Asp	Ile	Asn	Glu	Ala	Gly	Val	Arg	Val	Leu	Cys	Gln
5		180		185										190		
	Gly	Leu	Lys	Asp	Ser	Pro	Cys	Gln	Leu	Glu	Ala	Leu	Lys	Leu	Glu	Ser
		195		200									205			
	Cys	Gly	Val	Thr	Ser	Asp	Asn	Cys	Arg	Asp	Leu	Cys	Gly	Ile	Val	Ala
		210		215									220			
10	Ser	Lys	Ala	Ser	Leu	Arg	Glu	Leu	Ala	Leu	Gly	Ser	Asn	Lys	Leu	Gly
	225			230							235				240	
	Asp	Val	Gly	Met	Ala	Glu	Leu	Cys	Pro	Gly	Leu	Leu	His	Pro	Ser	Ser
			245							250				255		
	Arg	Leu	Arg	Thr	Leu	Trp	Ile	Trp	Glu	Cys	Gly	Ile	Thr	Ala	Lys	Gly
15		260		265										270		
	Cys	Gly	Asp	Leu	Cys	Arg	Val	Leu	Arg	Ala	Lys	Glu	Ser	Leu	Lys	Glu
		275		280										285		
	Leu	Ser	Leu	Ala	Gly	Asn	Glu	Leu	Gly	Asp	Glu	Gly	Ala	Arg	Leu	Leu
		290		295									300			
20	Cys	Glu	Thr	Leu	Leu	Glu	Pro	Gly	Cys	Gln	Leu	Glu	Ser	Leu	Trp	Val
	305			310							315				320	
	Lys	Ser	Cys	Ser	Phe	Thr	Ala	Ala	Cys	Cys	Ser	His	Phe	Ser	Ser	Val
			325							330				335		
	Leu	Ala	Gln	Asn	Arg	Phe	Leu	Leu	Glu	Leu	Gln	Ile	Ser	Asn	Asn	Arg

146/335

340 345 350  
Leu Glu Asp Ala Gly Val Arg Glu Leu Cys Gln Gly Leu Gly Gln Pro  
355 360 365  
Gly Ser Val Leu Arg Val Leu Trp Leu Ala Asp Cys Asp Val Ser Asp  
5 370 375 380  
Ser Ser Cys Ser Ser Leu Ala Ala Thr Leu Leu Ala Asn His Ser Leu  
385 390 395 400  
Arg Glu Leu Asp Leu Ser Asn Asn Cys Leu Gly Asp Ala Gly Ile Leu  
405 410 415  
10 Gln Leu Val Glu Ser Val Arg Gln Pro Gly Cys Leu Leu Glu Gln Leu  
420 425 430  
Val Leu Tyr Asp Ile Tyr Trp Ser Glu Glu Met Glu Asp Arg Leu Gln  
435 440 445  
Ala Leu Glu Lys Asp Lys Pro Ser Leu Arg Val Ile Ser  
15 450 455 460

&lt;210&gt; 47

&lt;211&gt; 317

20 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> Guanine nucleotide-binding protein beta subunit-like protein  
12.3

&lt;222&gt; (1)..(317)

&lt;223&gt; Accession No. as of 09 Dec 2002: P25388

&lt;400&gt; 47

5 Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly  
1 5 10 15  
Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu  
20 25 30  
Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp  
10 35 40 45  
Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His  
50 55 60  
Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser  
65 70 75 80  
15 Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr  
85 90 95  
Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala  
100 105 110  
Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr  
20 115 120 125  
Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp  
130 135 140  
Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser  
145 150 155 160

148/335

Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val  
165 170 175

Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr  
180 185 190

5 Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala  
195 200 205

Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly  
210 215 220

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys  
10 225 230 235 240

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile  
245 250 255

Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln  
260 265 270

15 Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser  
275 280 285

Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp  
290 295 300

Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg  
20 305 310 315

&lt;210&gt; 48

&lt;211&gt; 172

<212> PRT

<213> Homo sapiens

<220>

<221> Myosin regulatory light chain 2

5 <222> (1)..(172)

<223> Accession No. as of 10 Dec 2002: P24844

<400> 48

Met Ser Ser Lys Arg Ala Lys Ala Lys Thr Thr Lys Lys Arg Pro Gln  
10 1 5 10 15  
Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln  
20 25 30  
Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe  
35 40 45  
15 Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn  
50 55 60  
Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser Glu Ala Pro Gly Pro  
65 70 75 80  
Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly  
20 85 90 95  
Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu  
100 105 110  
Glu Ala Ser Gly Phe Ile His Glu Asp His Leu Arg Glu Leu Leu Thr  
115 120 125

150/335

Thr Met Gly Asp Arg Phe Thr Asp Glu Glu Val Asp Glu Met Tyr Arg  
130 135 140  
Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Val Glu Phe Thr  
145 150 155 160  
5 Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp  
165 170

<210> 49  
10 <211> 114  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> Calgranulin B  
15 <222> (1)..(114)  
<223> Accession No. as of 10 Dec 2002: P06702  
<400> 49

Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile  
20 1 5 10 15  
Asn Thr Phe His Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu  
20 25 30  
Asn Gln Gly Glu Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe  
35 40 45



151/335

Leu Lys Lys Glu Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu  
50 55 60  
Asp Leu Asp Thr Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile  
65 70 75 80  
5 Met Leu Met Ala Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu  
85 90 95  
Gly Asp Glu Gly Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly  
100 105 110  
Thr Pro

10

<210> 50  
<211> 348  
15 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Macrophage capping protein  
<222> (1)..(348)  
20 <223> Accession No. as of 10 Dec 2002: P40121  
<400> 50

Met Tyr Thr Ala Ile Pro Gln Ser Gly Ser Pro Phe Pro Gly Ser Val

1

5

10

15

152/335

Gln Asp Pro Gly Leu His Val Trp Arg Val Glu Lys Leu Lys Pro Val  
 20 25 30  
 Pro Val Ala Gln Glu Asn Gln Gly Val Phe Phe Ser Gly Asp Ser Tyr  
 35 40 45  
 5 Leu Val Leu His Asn Gly Pro Glu Glu Val Ser His Leu His Leu Trp  
 50 55 60  
 Ile Gly Gln Gln Ser Ser Arg Asp Glu Gln Gly Ala Cys Ala Val Leu  
 65 70 75 80  
 Ala Val His Leu Asn Thr Leu Leu Gly Glu Arg Pro Val Gln His Arg  
 10 85 90 95  
 Glu Val Gln Gly Asn Glu Ser Asp Leu Phe Met Ser Tyr Phe Pro Arg  
 100 105 110  
 Gly Leu Lys Tyr Gln Glu Gly Gly Val Glu Ser Ala Phe His Lys Thr  
 115 120 125  
 15 Ser Thr Gly Ala Pro Ala Ala Ile Lys Lys Leu Tyr Gln Val Lys Gly  
 130 135 140  
 Lys Lys Asn Ile Arg Ala Thr Glu Arg Ala Leu Asn Trp Asp Ser Phe  
 145 150 155 160  
 Asn Thr Gly Asp Cys Phe Ile Leu Asp Leu Gly Gln Asn Ile Phe Ala  
 20 165 170 175  
 Trp Cys Gly Gly Lys Ser Asn Ile Leu Glu Arg Asn Lys Ala Arg Asp  
 180 185 190  
 Leu Ala Leu Ala Ile Arg Asp Ser Glu Arg Gln Gly Lys Ala Gln Val  
 195 200 205

153/335

Glu Ile Val Thr Asp Gly Glu Glu Pro Ala Glu Met Ile Gln Val Leu  
210 215 220  
Gly Pro Lys Pro Ala Leu Lys Glu Gly Asn Pro Glu Glu Asp Leu Thr  
225 230 235 240  
5 Ala Asp Lys Ala Asn Ala Gln Ala Ala Ala Leu Tyr Lys Val Ser Asp  
245 250 255  
Ala Thr Gly Gln Met Asn Leu Thr Lys Val Ala Asp Ser Ser Pro Phe  
260 265 270  
Ala Leu Glu Leu Leu Ile Ser Asp Asp Cys Phe Val Leu Asp Asn Gly  
10 275 280 285  
Leu Cys Gly Lys Ile Tyr Ile Trp Lys Gly Arg Lys Ala Asn Glu Lys  
290 295 300  
Glu Arg Gln Ala Ala Leu Gln Val Ala Glu Gly Phe Ile Ser Arg Met  
305 310 315 320  
15 Gln Tyr Ala Pro Asn Thr Gln Val Glu Ile Leu Pro Gln Gly Arg Glu  
325 330 335  
Ser Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Lys  
340 345

20

&lt;210&gt; 51

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Annexin I

&lt;222&gt; (1)..(346)

&lt;223&gt; Accession No. as of 10 Dec 2002: P04083

5 &lt;400&gt; 51

Met Ala Met Val Ser Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn  
 1 5 10 15  
 Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro  
 10 20 25 30  
 Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val  
 35 40 45  
 Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr  
 50 55 60  
 15 Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile  
 65 70 75 80  
 Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu  
 85 90 95  
 Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu  
 20 100 105 110  
 Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys  
 115 120 125  
 Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg  
 130 135 140

155/335

Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu  
145 150 155 160  
Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe  
165 170 175  
5 Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe  
180 185 190  
Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu  
195 200 205  
Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile  
10 210 215 220  
Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr  
225 230 235 240  
Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu  
245 250 255  
15 Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr  
260 265 270  
Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly  
275 280 285  
Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser  
20 290 295 300  
Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly  
305 310 315 320  
Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu  
325 330 335

Lys Ile Leu Val Ala Leu Cys Gly Gly Asn

340

345

5 &lt;210&gt; 52

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

10 &lt;221&gt; Keratin, type II cytoskeletal 7

&lt;222&gt; (1)..(469)

&lt;223&gt; Accession No. as of 10 Dec 2002: P08729

&lt;400&gt; 52

15 Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala

1 5 10 15

Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly

20 25 30

Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg

20 35 40 45

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg

50 55 60

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala

65 70 75 80

157/335

Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys  
85 90 95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu  
100 105 110

5 Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu  
115 120 125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln  
130 135 140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly  
10 145 150 155 160

Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe  
165 170 175

Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn  
180 185 190

15 Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys  
195 200 205

Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe  
210 215 220

Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile  
20 225 230 235 240

Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp  
245 250 255

Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala  
260 265 270

158/335

Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu  
275 280 285

Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr  
290 295 300

5 Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala  
305 310 315 320

Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile  
325 330 335

Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala  
10 340 345 350

Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met  
355 360 365

Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala  
370 375 380

15 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
385 390 395 400

Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met  
405 410 415

Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu  
20 420 425 430

Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly  
435 440 445

Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg  
450 455 460



Arg Ser Ala Arg Asp

465

5 <210> 53

<211> 836

<212> PRT

<213> Homo sapiens

<220>

10 <221> Osteoblast specific factor 2 precursor

<222> (1)..(836)

<223> Accession No. as of 10 Dec 2002: Q15063

<400> 53

15 Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Ile Val

1 5 10 15

Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser

20 25 30

Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln

20 35 40 45

Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr

50 55 60

Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys

65 70 75 80

160/335

Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu  
85 90 95

Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr  
100 105 110

5 Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly  
115 120 125

Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn  
130 135 140

Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu  
10 145 150 155 160

Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr  
165 170 175

Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu  
180 185 190

15 Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys  
195 200 205

Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His  
210 215 220

Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe  
20 225 230 235 240

Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr  
245 250 255

Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe  
260 265 270

161/335

Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu  
275 280 285

Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His  
290 295 300

5 Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val  
305 310 315 320

Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp  
325 330 335

Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val  
10 340 345 350

Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp  
355 360 365

Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe  
370 375 380

15 Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp  
385 390 395 400

Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp  
405 410 415

Thr Leu Ser Met Val Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His  
20 420 425 430

Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile  
435 440 445

Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr  
450 455 460

162/335

Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly  
465 470 475 480  
Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu  
485 490 495  
5 Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe  
500 505 510  
Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro  
515 520 525  
Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met  
10 530 535 540  
Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln  
545 550 555 560  
Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly  
565 570 575  
15 Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys  
580 585 590  
Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys  
595 600 605  
Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val Val  
20 610 615 620  
Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu  
625 630 635 640  
Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val  
645 650 655

163/335

Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys  
660 665 670

Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser  
675 680 685

5 Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys  
690 695 700

Ile Glu Gly Glu Pro Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile  
705 710 715 720

Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile  
10 725 730 735

Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu  
740 745 750

Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly  
755 760 765

15 Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val  
770 775 780

Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu Phe Glu  
785 790 795 800

Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Arg Lys  
20 805 810 815

Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu Arg Glu  
820 825 830

Gly Arg Ser Gln  
835

<210> 54

<211> 687

5 <212> PRT

<213> Homo sapiens

<220>

<221> Protein-glutamine gamma-glutamyltransferase

<222> (1)..(687)

10 <223> Accession No. P21980

<400> 54

Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr

1 5 10 15

15 Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val

20 25 30

Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg

35 40 45

Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly

20 50 55 60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg

65 70 75 80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln

85 90 95

165/335

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile  
100 105 110  
Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser  
115 120 125  
5 Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro  
130 135 140  
Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val  
145 150 155 160  
Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys  
10 165 170 175  
Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile  
180 185 190  
Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly  
195 200 205  
15 Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val  
210 215 220  
Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg  
225 230 235 240  
Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly  
20 245 250 255  
Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val  
260 265 270  
Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu  
275 280 285

166/335

Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala  
290 295 300  
His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe  
305 310 315 320  
5 Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys  
325 330 335  
Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu  
340 345 350  
Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr  
10 355 360 365  
Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu  
370 375 380  
Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp  
385 390 395 400  
15 Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile  
405 410 415  
Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly  
420 425 430  
Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly  
20 435 440 445  
Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys  
450 455 460  
Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly  
465 470 475 480



167/335

Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr  
485 490 495

Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg  
500 505 510

5 Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr  
515 520 525

Leu Leu Asn Leu Asn Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu  
530 535 540

Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu  
10 545 550 555 560

Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu  
565 570 575

Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg  
580 585 590

15 Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser  
595 600 605

Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val  
610 615 620

Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp  
20 625 630 635 640

Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Leu Pro  
645 650 655

Leu His Met Gly Leu His Lys Leu Val Val Asn Phe Glu Ser Asp Lys  
660 665 670

168/335

Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala

675

680

685

5 &lt;210&gt; 55

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

10 &lt;221&gt; Rho GDP-dissociation inhibitor 1

&lt;222&gt; (1)..(204)

&lt;223&gt; Accession No. as of 10 Dec 2002: P52565

&lt;400&gt; 55

15 Met Ala Glu Gln Glu Pro Thr Ala Glu Gln Leu Ala Gln Ile Ala Ala

1

5

10

15

Glu Asn Glu Glu Asp Glu His Ser Val Asn Tyr Lys Pro Pro Ala Gln

20

25

30

Lys Ser Ile Gln Glu Ile Gln Glu Leu Asp Lys Asp Asp Glu Ser Leu

20

35

40

45

Arg Lys Tyr Lys Glu Ala Leu Leu Gly Arg Val Ala Val Ser Ala Asp

50

55

60

Pro Asn Val Pro Asn Val Val Val Thr Gly Leu Thr Leu Val Cys Ser

65

70

75

80

169/335

Ser Ala Pro Gly Pro Leu Glu Leu Asp Leu Thr Gly Asp Leu Glu Ser  
85 90 95  
Phe Lys Lys Gln Ser Phe Val Leu Lys Glu Gly Val Glu Tyr Arg Ile  
100 105 110  
5 Lys Ile Ser Phe Arg Val Asn Arg Glu Ile Val Ser Gly Met Lys Tyr  
115 120 125  
Ile Gln His Thr Tyr Arg Lys Gly Val Lys Ile Asp Lys Thr Asp Tyr  
130 135 140  
Met Val Gly Ser Tyr Gly Pro Arg Ala Glu Glu Tyr Glu Phe Leu Thr  
10 145 150 155 160  
Pro Val Glu Glu Ala Pro Lys Gly Met Leu Ala Arg Gly Ser Tyr Ser  
165 170 175  
Ile Lys Ser Arg Phe Thr Asp Asp Asp Lys Thr Asp His Leu Ser Trp  
180 185 190  
15 Glu Trp Asn Leu Thr Ile Lys Lys Asp Trp Lys Asp  
195 200

&lt;210&gt; 56

20 &lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Fascin 2

170/335

&lt;222&gt; (1) .. (492)

&lt;223&gt; Accession No. as of 29 August 2003: 014926

&lt;400&gt; 56

5 Met Pro Thr Asn Gly Leu His Gln Val Leu Lys Ile Gln Phe Gly Leu  
1 5 10 15  
Val Asn Asp Thr Asp Arg Tyr Leu Thr Ala Glu Ser Phe Gly Phe Lys  
20 25 30  
Val Asn Ala Ser Ala Pro Ser Leu Lys Arg Lys Gln Thr Trp Val Leu  
10 35 40 45  
Glu Pro Asp Pro Gly Gln Gly Thr Ala Val Leu Leu Arg Ser Ser His  
50 55 60  
Leu Gly Arg Tyr Leu Ser Ala Glu Glu Asp Gly Arg Val Ala Cys Glu  
65 70 75 80  
15 Ala Glu Gln Pro Gly Arg Asp Cys Arg Phe Leu Val Leu Pro Gln Pro  
85 90 95  
Asp Gly Arg Trp Val Leu Arg Ser Glu Pro His Gly Arg Phe Phe Gly  
100 105 110  
Gly Thr Glu Asp Gln Leu Ser Cys Phe Ala Thr Ala Val Ser Pro Ala  
20 115 120 125  
Glu Leu Trp Thr Val His Leu Ala Ile His Pro Gln Ala His Leu Leu  
130 135 140  
Ser Val Ser Arg Arg Arg Tyr Val His Leu Cys Pro Arg Glu Asp Glu  
145 150 155 160

171/335

Met Ala Ala Asp Gly Asp Lys Pro Trp Gly Val Asp Ala Leu Leu Thr  
165 170 175

Leu Ile Phe Arg Ser Arg Arg Tyr Cys Leu Lys Ser Cys Asp Ser Arg  
180 185 190

5 Tyr Leu Arg Ser Asp Gly Arg Leu Val Trp Glu Pro Glu Pro Arg Ala  
195 200 205

Cys Tyr Thr Leu Glu Phe Lys Ala Gly Lys Leu Ala Phe Lys Asp Cys  
210 215 220

Asp Gly His Tyr Leu Ala Pro Val Gly Pro Ala Gly Thr Leu Lys Ala  
10 225 230 235 240

Gly Arg Asn Thr Arg Pro Gly Lys Asp Glu Leu Phe Asp Leu Glu Glu  
245 250 255

Ser His Pro Gln Val Val Leu Val Ala Ala Asn His Arg Tyr Val Ser  
260 265 270

15 Val Arg Gln Gly Val Asn Val Ser Ala Asn Gln Asp Asp Glu Leu Asp  
275 280 285

His Glu Thr Phe Leu Met Gln Ile Asp Gln Glu Thr Lys Lys Cys Thr  
290 295 300

Phe Tyr Ser Ser Thr Gly Gly Tyr Trp Thr Leu Val Thr His Gly Gly  
20 305 310 315 320

Ile His Ala Thr Ala Thr Gln Val Ser Ala Asn Thr Met Phe Glu Met  
325 330 335

Glu Trp Arg Gly Arg Arg Val Ala Leu Lys Ala Ser Asn Gly Arg Tyr  
340 345 350

172/335

Val Cys Met Lys Lys Asn Gly Gln Leu Ala Ala Ile Ser Asp Phe Val  
355 360 365

Gly Lys Asp Glu Glu Phe Thr Leu Lys Leu Ile Asn Arg Pro Ile Leu  
370 375 380

5 Val Leu Arg Gly Leu Asp Gly Phe Val Cys His His Arg Gly Ser Asn  
385 390 395 400

Gln Leu Asp Thr Asn Arg Ser Val Tyr Asp Val Phe His Leu Ser Phe  
405 410 415

Ser Asp Gly Ala Tyr Arg Ile Arg Gly Arg Asp Gly Gly Phe Trp Tyr  
10 420 425 430

Thr Gly Ser His Gly Ser Val Cys Ser Asp Gly Glu Arg Ala Glu Asp  
435 440 445

Phe Val Phe Glu Phe Arg Glu Arg Gly Arg Leu Ala Ile Arg Ala Arg  
450 455 460

15 Ser Gly Lys Tyr Leu Arg Gly Gly Ala Ser Gly Leu Leu Arg Ala Asp  
465 470 475 480

Ala Asp Ala Pro Ala Gly Thr Ala Leu Trp Glu Tyr  
485 490

20

&lt;210&gt; 57

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Destrin (Actin-depolymerizing factor) (ADF)

&lt;222&gt; (1)..(165)

&lt;223&gt; Accession No. as of 29 August 2003: P18282

5 &lt;400&gt; 57

Met Ala Ser Gly Val Gln Val Ala Asp Glu Val Cys Arg Ile Phe Tyr  
1 5 10 15  
Asp Met Lys Val Arg Lys Cys Ser Thr Pro Glu Glu Ile Lys Lys Arg  
10 20 25 30  
Lys Lys Ala Val Ile Phe Cys Leu Ser Ala Asp Lys Lys Cys Ile Ile  
35 40 45  
Val Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Val Thr Ile  
50 55 60  
15 Thr Asp Pro Phe Lys His Phe Val Gly Met Leu Pro Glu Lys Asp Cys  
65 70 75 80  
Arg Tyr Ala Leu Tyr Asp Ala Ser Phe Glu Thr Lys Glu Ser Arg Lys  
85 90 95  
Glu Glu Leu Met Phe Phe Leu Trp Ala Pro Glu Leu Ala Pro Leu Lys  
20 100 105 110  
Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Phe  
115 120 125  
Gln Gly Ile Lys His Glu Cys Gln Ala Asn Gly Pro Glu Asp Leu Asn  
130 135 140

174/335

Arg Ala Cys Ile Ala Glu Lys Leu Gly Gly Ser Leu Ile Val Ala Phe

145

150

155

160

Glu Gly Cys Pro Val

165

5

&lt;210&gt; 58

&lt;211&gt; 492

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Fascin

&lt;222&gt; (1)..(492)

&lt;223&gt; Accession No. as of 29 August 2003: Q16658

15 &lt;400&gt; 58

Thr Ala Asn Gly Thr Ala Glu Ala Val Gln Ile Gln Phe Gly Leu Ile

1

5

10

15

Asn Cys Gly Asn Lys Tyr Leu Thr Ala Glu Ala Phe Gly Phe Lys Val

20

20

25

30

Asn Ala Ser Ala Ser Ser Leu Lys Lys Lys Gln Ile Trp Thr Leu Glu

35

40

45

Gln Pro Pro Asp Glu Ala Gly Ser Ala Ala Val Cys Leu Arg Ser His

50

55

60



175/335

Leu Gly Arg Tyr Leu Ala Ala Asp Lys Asp Gly Asn Val Thr Cys Glu  
65 70 75 80  
Arg Glu Val Pro Gly Pro Asp Cys Arg Phe Leu Ile Val Ala His Asp  
85 90 95  
5 Asp Gly Arg Trp Ser Leu Gln Ser Glu Ala His Arg Arg Tyr Phe Gly  
100 105 110  
Gly Thr Glu Asp Arg Leu Ser Cys Phe Ala Gln Thr Val Ser Pro Ala  
115 120 125  
Glu Lys Trp Ser Val His Ile Ala Met His Pro Gln Val Asn Ile Tyr  
10 130 135 140  
Ser Val Thr Arg Lys Arg Tyr Ala His Leu Ser Ala Arg Pro Ala Asp  
145 150 155 160  
Glu Ile Ala Val Asp Arg Asp Val Pro Trp Gly Val Asp Ser Leu Ile  
165 170 175  
15 Thr Leu Ala Phe Gln Asp Gln Arg Tyr Ser Val Gln Thr Ala Asp His  
180 185 190  
Arg Phe Leu Arg His Asp Gly Arg Leu Val Ala Arg Pro Glu Pro Ala  
195 200 205  
Thr Gly Tyr Thr Leu Glu Phe Arg Ser Gly Lys Val Ala Phe Arg Asp  
20 210 215 220  
Cys Glu Gly Arg Tyr Leu Ala Pro Ser Gly Pro Ser Gly Thr Leu Lys  
225 230 235 240  
Ala Gly Lys Ala Thr Lys Val Gly Lys Asp Glu Leu Phe Ala Leu Glu  
245 250 255

176/335

Gln Ser Cys Ala Gln Val Val Leu Gln Ala Ala Asn Glu Arg Asn Val  
260 265 270

Ser Thr Arg Gln Gly Met Asp Leu Ser Ala Asn Gln Asp Glu Glu Thr  
275 280 285

5 Asp Gln Glu Thr Phe Gln Leu Glu Ile Asp Arg Asp Thr Lys Lys Cys  
290 295 300

Ala Phe Arg Thr His Thr Gly Lys Tyr Trp Thr Leu Thr Ala Thr Gly  
305 310 315 320

Gly Val Gln Ser Thr Ala Ser Ser Lys Asn Ala Ser Cys Tyr Phe Asp  
10 325 330 335

Ile Glu Trp Arg Asp Arg Arg Ile Thr Leu Arg Ala Ser Asn Gly Lys  
340 345 350

Phe Val Thr Ser Lys Lys Asn Gly Gln Leu Ala Ala Ser Val Glu Thr  
355 360 365

15 Ala Gly Asp Ser Glu Leu Phe Leu Met Lys Leu Ile Asn Arg Pro Ile  
370 375 380

Ile Val Phe Arg Gly Glu His Gly Phe Ile Gly Cys Arg Lys Val Thr  
385 390 395 400

Gly Thr Leu Asp Ala Asn Arg Ser Ser Tyr Asp Val Phe Gln Leu Glu  
20 405 410 415

Phe Asn Asp Gly Ala Tyr Asn Ile Lys Asp Ser Thr Gly Lys Tyr Trp  
420 425 430

Thr Val Gly Ser Asp Ser Ala Val Thr Ser Ser Gly Asp Thr Pro Val  
435 440 445

177/335

Asp Phe Phe Phe Glu Phe Cys Asp Tyr Asn Lys Val Ala Ile Lys Val  
450 455 460  
Gly Gly Arg Tyr Leu Lys Gly Asp His Ala Gly Val Leu Lys Ala Ser  
465 470 475 480  
5 Ala Glu Thr Val Asp Pro Ala Ser Leu Trp Glu Tyr  
485 490

<210> 59  
10 <211> 317  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> Apo-E precursor  
15 <222> (1)..(317)  
<223> Accession No. as of 29 August 2003: P02649  
<400> 59

Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys  
20 1 5 10 15  
Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu  
20 25 30  
Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu  
35 40 45

178/335

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln  
50 55 60  
Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala  
65 70 75 80  
5 Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu  
85 90 95  
Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser  
100 105 110  
Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp  
10 115 120 125  
Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu  
130 135 140  
Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg  
145 150 155 160  
15 Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg  
165 170 175  
Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu  
180 185 190  
Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val  
20 195 200 205  
Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg  
210 215 220  
Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly  
225 230 235 240

179/335

Ser Arg Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu  
245 250 255  
Val Arg Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala  
260 265 270  
5 Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu  
275 280 285  
Asp Met Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala  
290 295 300  
Val Gly Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His  
10 305 310 315

<210> 60  
<211> 838  
15 <212> PRT  
<213> Homo sapiens  
<220>  
<221> hypothetical 88.6 kDa protein  
<222> (1)..(838)  
20 <223> Accession No. as of 29 August 2003: Q96C61  
<400> 60

Met Pro Ser Gly Lys Val Ala Gln Pro Thr Ile Thr Asp Asn Lys Asp

1

5

10

15

180/335

Gly Thr Val Thr Val Arg Tyr Ala Pro Ser Glu Ala Gly Leu His Glu  
20 25 30  
Met Asp Ile Arg Tyr Asp Asn Met His Ile Pro Gly Ser Pro Leu Gln  
35 40 45  
5 Phe Tyr Val Asp Tyr Val Asn Cys Gly His Val Thr Ala Tyr Gly Pro  
50 55 60  
Gly Leu Thr His Gly Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn  
65 70 75 80  
Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro  
10 85 90 95  
Ser Lys Ala Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser  
100 105 110  
Val Ser Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys  
115 120 125  
15 Tyr Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr  
130 135 140  
Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala Ala  
145 150 155 160  
Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu Thr Ala  
20 165 170 175  
Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu Leu Lys Arg  
180 185 190  
Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr Gly  
195 200 205

181/335

Glu His Leu Val His Val Lys Lys Asn Gly Gln His Val Ala Ser Ser  
 210 215 220  
 Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser Arg  
 225 230 235 240  
 5 Val Arg Val Ser Gly Gln Gly Leu His Glu Gly His Thr Phe Glu Pro  
 245 250 255  
 Ala Glu Phe Ile Ile Asp Thr Arg Asp Ala Gly Tyr Gly Gly Leu Ser  
 260 265 270  
 Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp Leu  
 10 275 280 285  
 Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Glu Pro Gly Asn  
 290 295 300  
 Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser Pro  
 305 310 315 320  
 15 Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile Thr  
 325 330 335  
 Arg Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys Asp  
 340 345 350  
 Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala Gln  
 20 355 360 365  
 Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu Gly  
 370 375 380  
 Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly Thr  
 385 390 395 400

182/335

His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser Pro  
405 410 415

Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala His Lys Val  
420 425 430

5 Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro Ala  
435 440 445

Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Gly Leu Ala Ile  
450 455 460

Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg Lys  
10 465 470 475 480

Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Glu Pro Gly Asp Tyr  
485 490 495

Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro Phe  
500 505 510

15 Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr Val  
515 520 525

Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser Phe  
530 535 540

Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val His  
20 545 550 555 560

Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp Gln  
565 570 575

Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr Leu  
580 585 590



Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe Lys  
595 600 605

Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val Ser  
610 615 620

5 Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala Glu  
625 630 635 640

Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val Thr  
645 650 655

Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu  
10 660 665 670

Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile  
675 680 685

Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys  
690 695 700

15 Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu  
705 710 715 720

Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro  
725 730 735

Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val  
20 740 745 750

Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser Ser  
755 760 765

Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val Gly  
770 775 780

184/335

Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His Val

785                      790                      795                      800

Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly Glu

805                      810                      815

5 Tyr Thr Leu Val Val Lys Trp Gly Asp Glu His Ile Pro Gly Ser Pro

820                      825                      830

Tyr Arg Val Val Val Pro

835

10

<210> 61

<211> 433

<212> PRT

<213> Homo sapiens

15 <220>

<221> human alpha enolase

<222> (1)..(433)

<223> Accession No. as of 29 August 2003: P06733

<400> 61

20

Ser Ile Leu Lys Ile His Ala Arg Glu Ile Phe Asp Ser Arg Gly Asn

1                      5                      10                      15

Pro Thr Val Glu Val Asp Leu Phe Thr Ser Lys Gly Leu Phe Arg Ala

20                      25                      30

185/335

Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu  
35 40 45

Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Lys Gly Val Ser Lys Ala  
50 55 60

5 Val Glu His Ile Asn Lys Thr Ile Ala Pro Ala Leu Val Ser Lys Lys  
65 70 75 80

Leu Asn Val Thr Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met  
85 90 95

Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly  
10 100 105 110

Val Ser Leu Ala Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro  
115 120 125

Leu Tyr Arg His Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu  
130 135 140

15 Pro Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn  
145 150 155 160

Lys Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn  
165 170 175

Phe Arg Glu Ala Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys  
20 180 185 190

Asn Val Ile Lys Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp  
195 200 205

Glu Gly Gly Phe Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu  
210 215 220

186/335

Leu Leu Lys Thr Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val  
225 230 235 240  
Ile Gly Met Asp Val Ala Ala Ser Glu Phe Phe Arg Ser Gly Lys Tyr  
245 250 255  
5 Asp Leu Asp Phe Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro  
260 265 270  
Asp Gln Leu Ala Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val  
275 280 285  
Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln  
10 290 295 300  
Lys Phe Thr Ala Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr  
305 310 315 320  
Val Thr Asn Pro Lys Arg Ile Ala Lys Ala Val Asn Glu Lys Ser Cys  
325 330 335  
15 Asn Cys Leu Leu Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser  
340 345 350  
Leu Gln Ala Cys Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val  
355 360 365  
Ser His Arg Ser Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val  
20 370 375 380  
Val Gly Leu Cys Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser  
385 390 395 400  
Glu Arg Leu Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu  
405 410 415

187/335

Gly Ser Lys Ala Lys Phe Ala Gly Arg Asn Phe Arg Asn Pro Leu Ala

420

425

430

Lys

5

&lt;210&gt; 62

&lt;211&gt; 471

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; tryptophanyl-tRNA synthetase

&lt;222&gt; (1)..(471)

&lt;223&gt; Accession No. as of 29 August 2003: P23381

15 &lt;400&gt; 62

Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile

1

5

10

15

Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser

20

20

25

30

Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met

35

40

45

Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro

50

55

60

188/335

Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala  
65 70 75 80  
Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys  
85 90 95  
5 Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile  
100 105 110  
Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro  
115 120 125  
His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn  
10 130 135 140  
Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr  
145 150 155 160  
Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro  
165 170 175  
15 Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val  
180 185 190  
Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu  
195 200 205  
Asp Gln Ala Tyr Ser Tyr Ala Val Glu Asn Ala Lys Asp Ile Ile Ala  
20 210 215 220  
Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr  
225 230 235 240  
Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys  
245 250 255

189/335

His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser  
260 265 270

Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser  
275 280 285

5 Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln  
290 295 300

Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr  
305 310 315 320

Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His  
10 325 330 335

Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala  
340 345 350

Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile  
355 360 365

15 Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile  
370 375 380

Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe  
385 390 395 400

Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile  
20 405 410 415

Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys  
420 425 430

Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg  
435 440 445

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg

450

455

460

Lys Leu Ser Phe Asp Phe Gln

465

470

5

&lt;210&gt; 63

&lt;211&gt; 106

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Ig kappa chain C regionI

&lt;222&gt; (1)..(106)

&lt;223&gt; Accession No. as of 29 August 2003: P01834

15 &lt;400&gt; 63

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

1

5

10

15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr

20

20

25

30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

35

40

45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr

50

55

60



191/335

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

65

70

75

80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro

85

90

95

5 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

100

105

&lt;210&gt; 64

10 &lt;211&gt; 758

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Mitofilin

15 &lt;222&gt; (1)..(758)

&lt;223&gt; Accession No. as of 29 August 2003: Q16891

&lt;400&gt; 64

Met Leu Arg Ala Cys Gln Leu Ser Gly Val Thr Ala Ala Ala Gln Ser

20

1

5

10

15

Cys Leu Cys Gly Lys Phe Val Leu Arg Pro Leu Arg Pro Cys Arg Arg

20

25

30

Tyr Ser Thr Ser Gly Ser Ser Gly Leu Thr Thr Gly Lys Ile Ala Gly

35

40

45

192/335

Ala Gly Leu Leu Phe Val Gly Gly Gly Ile Gly Gly Thr Ile Leu Tyr  
50 55 60

Ala Lys Trp Asp Ser His Phe Arg Glu Ser Val Glu Lys Thr Ile Pro  
65 70 75 80

5 Tyr Ser Asp Lys Leu Phe Glu Met Val Leu Gly Pro Ala Ala Tyr Asn  
85 90 95

Val Pro Leu Pro Lys Lys Ser Ile Gln Ser Gly Pro Leu Lys Ile Ser  
100 105 110

Ser Val Ser Glu Val Met Lys Glu Ser Lys Gln Pro Ala Ser Gln Leu  
10 115 120 125

Gln Lys Gln Lys Gly Asp Thr Pro Ala Ser Ala Thr Ala Pro Thr Glu  
130 135 140

Ala Ala Gln Ile Ile Ser Ala Ala Gly Asp Thr Leu Ser Val Pro Ala  
145 150 155 160

15 Pro Ala Val Gln Pro Glu Glu Ser Leu Lys Thr Asp His Pro Glu Ile  
165 170 175

Gly Glu Gly Lys Pro Thr Pro Ala Leu Ser Glu Glu Ala Ser Ser Ser  
180 185 190

Ser Ile Arg Glu Arg Pro Pro Glu Glu Val Ala Ala Arg Leu Ala Gln  
20 195 200 205

Gln Glu Lys Gln Glu Gln Val Lys Ile Glu Ser Leu Ala Lys Ser Leu  
210 215 220

Glu Asp Ala Leu Arg Gln Thr Ala Ser Val Thr Leu Gln Ala Ile Ala  
225 230 235 240

193/335

Ala Gln Asn Ala Ala Val Gln Ala Val Asn Ala His Ser Asn Ile Leu  
245 250 255

Lys Ala Ala Met Asp Asn Ser Glu Ile Ala Gly Glu Lys Lys Ser Ala  
260 265 270

5 Gln Trp Arg Thr Val Glu Gly Ala Leu Lys Glu Arg Arg Lys Ala Val  
275 280 285

Asp Glu Ala Ala Asp Ala Leu Leu Lys Ala Lys Glu Glu Leu Glu Lys  
290 295 300

Met Lys Ser Val Ile Glu Asn Ala Lys Lys Lys Glu Val Ala Gly Ala  
10 305 310 315 320

Lys Pro His Ile Thr Ala Ala Glu Gly Lys Leu His Asn Met Ile Val  
325 330 335

Asp Leu Asp Asn Val Val Lys Lys Val Gln Ala Ala Gln Ser Glu Ala  
340 345 350

15 Lys Val Val Ser Gln Tyr His Glu Leu Val Val Gln Ala Arg Asp Asp  
355 360 365

Phe Lys Arg Glu Leu Asp Ser Ile Thr Pro Glu Val Leu Pro Gly Trp  
370 375 380

Lys Gly Met Ser Val Ser Asp Leu Ala Asp Lys Leu Ser Thr Asp Asp  
20 385 390 395 400

Leu Asn Ser Leu Ile Ala His Ala His Arg Arg Ile Asp Gln Leu Asn  
405 410 415

Arg Glu Leu Ala Glu Gln Lys Ala Thr Glu Lys Gln His Ile Thr Leu  
420 425 430

194/335

Ala Leu Glu Lys Gln Lys Leu Glu Glu Lys Arg Ala Phe Asp Ser Ala  
435 440 445

Val Ala Lys Ala Leu Glu His His Arg Ser Glu Ile Gln Ala Glu Gln  
450 455 460

5 Asp Arg Lys Ile Glu Glu Val Arg Asp Ala Met Glu Asn Glu Met Arg  
465 470 475 480

Thr Gln Leu Arg Arg Gln Ala Ala Ala His Thr Asp His Leu Arg Asp  
485 490 495

Val Leu Arg Val Gln Glu Gln Glu Leu Lys Ser Glu Phe Glu Gln Asn  
10 500 505 510

Leu Ser Glu Lys Leu Ser Glu Gln Glu Leu Gln Phe Arg Arg Leu Ser  
515 520 525

Gln Glu Gln Val Asp Asn Phe Thr Leu Asp Ile Asn Thr Ala Tyr Ala  
530 535 540

15 Arg Leu Arg Gly Ile Glu Gln Ala Val Gln Ser His Ala Val Ala Glu  
545 550 555 560

Glu Glu Ala Arg Lys Ala His Gln Leu Trp Leu Ser Val Glu Ala Leu  
565 570 575

Lys Tyr Ser Met Lys Thr Ser Ser Ala Glu Thr Pro Thr Ile Pro Leu  
20 580 585 590

Gly Ser Ala Val Glu Ala Ile Lys Ala Asn Cys Ser Asp Asn Glu Phe  
595 600 605

Thr Gln Ala Leu Thr Ala Ala Ile Pro Pro Glu Ser Leu Thr Arg Gly  
610 615 620

195/335

Val Tyr Ser Glu Glu Thr Leu Arg Ala Arg Phe Tyr Ala Val Gln Lys  
625 630 635 640  
Leu Ala Arg Arg Val Ala Met Ile Asp Glu Thr Arg Asn Ser Leu Tyr  
645 650 655  
5 Gln Tyr Phe Leu Ser Tyr Leu Gln Ser Leu Leu Leu Phe Pro Pro Gln  
660 665 670  
Gln Leu Lys Pro Pro Pro Glu Leu Cys Pro Glu Asp Ile Asn Thr Phe  
675 680 685  
Lys Leu Leu Ser Tyr Ala Ser Tyr Cys Ile Glu His Gly Asp Leu Glu  
10 690 695 700  
Leu Ala Ala Lys Phe Val Asn Gln Leu Lys Gly Glu Ser Arg Arg Val  
705 710 715 720  
Ala Gln Asp Trp Leu Lys Glu Ala Arg Met Thr Leu Glu Thr Lys Gln  
725 730 735  
15 Ile Val Glu Ile Leu Thr Ala Tyr Ala Ser Ala Val Gly Ile Gly Thr  
740 745 750  
Thr Gln Val Gln Pro Glu  
755

20

&lt;210&gt; 65

&lt;211&gt; 1410

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Ribosome-binding protein 1

&lt;222&gt; (1)..(1410)

&lt;223&gt; Accession No. as of 29 August 2003: 075300

5 &lt;400&gt; 65

Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly  
1 5 10 15  
Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser  
10 20 25 30  
Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu  
35 40 45  
Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys  
50 55 60  
15 Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn  
65 70 75 80  
Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu  
85 90 95  
Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val  
20 100 105 110  
Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro  
115 120 125  
Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys  
130 135 140

197/335

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile  
145 150 155 160  
Gln Val Leu Thr Ser Lys Ala Ala Ile Leu Glu Thr Ala Pro Lys Glu  
165 170 175  
5 Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro  
180 185 190  
Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln  
195 200 205  
Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly  
10 210 215 220  
Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys  
225 230 235 240  
Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro  
245 250 255  
15 Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val  
260 265 270  
Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln  
275 280 285  
Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly  
20 290 295 300  
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys  
305 310 315 320  
Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln  
325 330 335

198/335

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala  
340 345 350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln  
355 360 365

5 Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ser Glu Gly  
370 375 380

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys  
385 390 395 400

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln  
10 405 410 415

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala  
420 425 430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln  
435 440 445

15 Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly  
450 455 460

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys  
465 470 475 480

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln  
20 485 490 495

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln Lys Gly  
500 505 510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln Gly Lys  
515 520 525



Lys Ala Glu Arg Ser Pro Asn Gln Gly Lys Lys Gly Glu Gly Ala Pro  
530 535 540  
Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr Lys Val  
545 550 555 560  
5 Glu Gly Ile Thr Asn Gln Gly Lys Lys Ala Glu Gly Ser Pro Ser Glu  
565 570 575  
Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala Asp Ala  
580 585 590  
Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln Gly Arg  
10 595 600 605  
Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu Ala Pro  
610 615 620  
Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly Pro Pro  
625 630 635 640  
15 Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr  
645 650 655  
Val Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu  
660 665 670  
Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala  
20 675 680 685  
Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu  
690 695 700  
Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys  
705 710 715 720

200/335

Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys  
725 730 735

Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu  
740 745 750

5 Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu  
755 760 765

His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln  
770 775 780

Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln  
10 785 790 795 800

Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val  
805 810 815

Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser  
820 825 830

15 Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg Gln Asp  
835 840 845

Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys  
850 855 860

Gln Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu  
20 865 870 875 880

Gln Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys His Thr Gln Ser  
885 890 895

Ser His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln  
900 905 910

201/335

Gln Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu  
915 920 925

Val Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln  
930 935 940

5 Glu Ala Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile  
945 950 955 960

Glu Ala Leu Leu Glu Ala Gly Gln Ala Arg Asp Ala Gln Asp Val Gln  
965 970 975

Ala Ser Gln Ala Glu Ala Asp Gln Gln Gln Thr Arg Leu Lys Glu Leu  
10 980 985 990

Glu Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Ile Glu Leu Arg Glu  
995 1000 1005

Ala Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys  
1010 1015 1020

15 Asn Trp Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys  
1025 1030 1035

Lys Glu Lys Leu Leu Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu  
1040 1045 1050

Lys Gln Leu Cys Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu  
20 1055 1060 1065

Ala Leu Leu Pro Glu Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr  
1070 1075 1080

Glu Trp Leu Gln Asp Leu Lys Glu Lys Gly Pro Thr Leu Leu Lys  
1085 1090 1095

202/335

	His	Pro	Pro	Ala	Pro	Ala	Glu	Pro	Ser	Ser	Asp	Leu	Ala	Ser	Lys
	1100						1105					1110			
	Leu	Arg	Glu	Ala	Glu	Glu	Thr	Gln	Ser	Thr	Leu	Gln	Ala	Glu	Cys
	1115						1120					1125			
5	Asp	Gln	Tyr	Arg	Ser	Ile	Leu	Ala	Glu	Thr	Glu	Gly	Met	Leu	Arg
	1130						1135					1140			
	Asp	Leu	Gln	Lys	Ser	Val	Glu	Glu	Glu	Glu	Gln	Val	Trp	Arg	Ala
	1145						1150					1155			
	Lys	Val	Gly	Ala	Ala	Glu	Glu	Glu	Leu	Gln	Lys	Ser	Arg	Val	Thr
10	1160						1165					1170			
	Val	Lys	His	Leu	Glu	Glu	Ile	Val	Glu	Lys	Leu	Lys	Gly	Glu	Leu
	1175						1180					1185			
	Glu	Ser	Ser	Asp	Gln	Val	Arg	Glu	His	Thr	Ser	His	Leu	Glu	Ala
	1190						1195					1200			
15	Glu	Leu	Glu	Lys	His	Met	Ala	Ala	Ala	Ser	Ala	Glu	Cys	Gln	Asn
	1205						1210					1215			
	Tyr	Ala	Lys	Glu	Val	Ala	Gly	Leu	Arg	Gln	Leu	Leu	Leu	Glu	Ser
	1220						1225					1230			
	Gln	Ser	Gln	Leu	Asp	Ala	Ala	Lys	Ser	Glu	Ala	Gln	Lys	Gln	Ser
20	1235						1240					1245			
	Asp	Glu	Leu	Ala	Leu	Val	Arg	Gln	Gln	Leu	Ser	Glu	Met	Lys	Ser
	1250						1255					1260			
	His	Val	Glu	Asp	Gly	Asp	Ile	Ala	Gly	Ala	Pro	Ala	Ser	Ser	Pro
	1265						1270					1275			

Glu Ala Pro Pro Ala Glu Gln Asp Pro Val Gln Leu Lys Thr Gln  
1280 1285 1290

Leu Glu Trp Thr Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg  
1295 1300 1305

5 Gln Lys Leu Thr Ala Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys  
1310 1315 1320

Arg Leu Gln Glu Glu Leu Glu Lys Leu Arg Thr Ala Gly Pro Leu  
1325 1330 1335

Glu Ser Ser Glu Thr Glu Glu Ala Ser Gln Leu Lys Glu Arg Leu  
10 1340 1345 1350

Glu Lys Glu Lys Lys Leu Thr Ser Asp Leu Gly Arg Ala Ala Thr  
1355 1360 1365

Arg Leu Gln Glu Leu Leu Lys Thr Thr Gln Glu Gln Leu Ala Arg  
1370 1375 1380

15 Glu Lys Asp Thr Val Lys Lys Leu Gln Glu Gln Leu Glu Lys Ala  
1385 1390 1395

Glu Asp Gly Ser Ser Ser Lys Glu Gly Thr Ser Val  
1400 1405 1410

20

&lt;210&gt; 66

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Fibrinogen gamma chain precursor

&lt;222&gt; (1)..(453)

&lt;223&gt; Accession No. as of 29 August 2003: P02679

5 &lt;400&gt; 66

Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala  
1 5 10 15  
Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp  
10 20 25 30  
Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr  
35 40 45  
Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys  
50 55 60  
15 Asp Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr  
65 70 75 80  
Ser Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro  
85 90 95  
Asp Glu Ser Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser  
20 100 105 110  
Arg Lys Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile Leu Thr  
115 120 125  
His Asp Ser Ser Ile Arg Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn  
130 135 140

205/335

Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln  
145 150 155 160  
Cys Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly  
165 170 175  
5 Lys Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu  
180 185 190  
Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys  
195 200 205  
Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys Arg Leu  
10 210 215 220  
Asp Gly Ser Val Asp Phe Lys Lys Asn Trp Ile Gln Tyr Lys Glu Gly  
225 230 235 240  
Phe Gly His Leu Ser Pro Thr Gly Thr Thr Glu Phe Trp Leu Gly Asn  
245 250 255  
15 Glu Lys Ile His Leu Ile Ser Thr Gln Ser Ala Ile Pro Tyr Ala Leu  
260 265 270  
Arg Val Glu Leu Glu Asp Trp Asn Gly Arg Thr Ser Thr Ala Asp Tyr  
275 280 285  
Ala Met Phe Lys Val Gly Pro Glu Ala Asp Lys Tyr Arg Leu Thr Tyr  
20 290 295 300  
Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp Ala Phe Asp Gly Phe Asp  
305 310 315 320  
Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe Thr Ser His Asn Gly Met  
325 330 335

206/335

Gln Phe Ser Thr Trp Asp Asn Asp Asn Asp Lys Phe Glu Gly Asn Cys  
340 345 350  
Ala Glu Gln Asp Gly Ser Gly Trp Trp Met Asn Lys Cys His Ala Gly  
355 360 365  
5 His Leu Asn Gly Val Tyr Tyr Gln Gly Gly Thr Tyr Ser Lys Ala Ser  
370 375 380  
Thr Pro Asn Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr  
385 390 395 400  
Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn  
10 405 410 415  
Arg Leu Thr Ile Gly Glu Gly Gln Gln His His Leu Gly Gly Ala Lys  
420 425 430  
Gln Val Arg Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr  
435 440 445  
15 Pro Glu Asp Asp Leu  
450

&lt;210&gt; 67

20 &lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Prothrombin precursor



&lt;222&gt; (1)..(622)

&lt;223&gt; Accession No. as of 29 August 2003: P00734

&lt;400&gt; 67

5 Met Ala His Val Arg Gly Leu Gln Leu Pro Gly Cys Leu Ala Leu Ala  
1 5 10 15  
Ala Leu Cys Ser Leu Val His Ser Gln His Val Phe Leu Ala Pro Gln  
20 25 30  
Gln Ala Arg Ser Leu Leu Gln Arg Val Arg Arg Ala Asn Thr Phe Leu  
10 35 40 45  
Glu Glu Val Arg Lys Gly Asn Leu Glu Arg Glu Cys Val Glu Glu Thr  
50 55 60  
Cys Ser Tyr Glu Glu Ala Phe Glu Ala Leu Glu Ser Ser Thr Ala Thr  
65 70 75 80  
15 Asp Val Phe Trp Ala Lys Tyr Thr Ala Cys Glu Thr Ala Arg Thr Pro  
85 90 95  
Arg Asp Lys Leu Ala Ala Cys Leu Glu Gly Asn Cys Ala Glu Gly Leu  
100 105 110  
Gly Thr Asn Tyr Arg Gly His Val Asn Ile Thr Arg Ser Gly Ile Glu  
20 115 120 125  
Cys Gln Leu Trp Arg Ser Arg Tyr Pro His Lys Pro Glu Ile Asn Ser  
130 135 140  
Thr Thr His Pro Gly Ala Asp Leu Gln Glu Asn Phe Cys Arg Asn Pro  
145 150 155 160

Asp Ser Ser Thr Thr Gly Pro Trp Cys Tyr Thr Thr Asp Pro Thr Val  
 165 170 175  
 Arg Arg Gln Glu Cys Ser Ile Pro Val Cys Gly Gln Asp Gln Val Thr  
 180 185 190  
 5 Val Ala Met Thr Pro Arg Ser Glu Gly Ser Ser Val Asn Leu Ser Pro  
 195 200 205  
 Pro Leu Glu Gln Cys Val Pro Asp Arg Gly Gln Gln Tyr Gln Gly Arg  
 210 215 220  
 Leu Ala Val Thr Thr His Gly Leu Pro Cys Leu Ala Trp Ala Ser Ala  
 10 225 230 235 240  
 Gln Ala Lys Ala Leu Ser Lys His Gln Asp Phe Asn Ser Ala Val Gln  
 245 250 255  
 Leu Val Glu Asn Phe Cys Arg Asn Pro Asp Gly Asp Glu Glu Gly Val  
 260 265 270  
 15 Trp Cys Tyr Val Ala Gly Lys Pro Gly Asp Phe Gly Tyr Cys Asp Leu  
 275 280 285  
 Asn Tyr Cys Glu Glu Ala Val Glu Glu Glu Thr Gly Asp Gly Leu Asp  
 290 295 300  
 Glu Asp Ser Asp Arg Ala Ile Glu Gly Arg Thr Ala Thr Ser Glu Tyr  
 20 305 310 315 320  
 Gln Thr Phe Phe Asn Pro Arg Thr Phe Gly Ser Gly Glu Ala Asp Cys  
 325 330 335  
 Gly Leu Arg Pro Leu Phe Glu Lys Lys Ser Leu Glu Asp Lys Thr Glu  
 340 345 350

209/335

Arg Glu Leu Leu Glu Ser Tyr Ile Asp Gly Arg Ile Val Glu Gly Ser  
355 360 365

Asp Ala Glu Ile Gly Met Ser Pro Trp Gln Val Met Leu Phe Arg Lys  
370 375 380

5 Ser Pro Gln Glu Leu Leu Cys Gly Ala Ser Leu Ile Ser Asp Arg Trp  
385 390 395 400

Val Leu Thr Ala Ala His Cys Leu Leu Tyr Pro Pro Trp Asp Lys Asn  
405 410 415

Phe Thr Glu Asn Asp Leu Leu Val Arg Ile Gly Lys His Ser Arg Thr  
10 420 425 430

Arg Tyr Glu Arg Asn Ile Glu Lys Ile Ser Met Leu Glu Lys Ile Tyr  
435 440 445

Ile His Pro Arg Tyr Asn Trp Arg Glu Asn Leu Asp Arg Asp Ile Ala  
450 455 460

15 Leu Met Lys Leu Lys Lys Pro Val Ala Phe Ser Asp Tyr Ile His Pro  
465 470 475 480

Val Cys Leu Pro Asp Arg Glu Thr Ala Ala Ser Leu Leu Gln Ala Gly  
485 490 495

Tyr Lys Gly Arg Val Thr Gly Trp Gly Asn Leu Lys Glu Thr Trp Thr  
20 500 505 510

Ala Asn Val Gly Lys Gly Gln Pro Ser Val Leu Gln Val Val Asn Leu  
515 520 525

Pro Ile Val Glu Arg Pro Val Cys Lys Asp Ser Thr Arg Ile Arg Ile  
530 535 540

210/335

Thr Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg  
545 550 555 560  
Gly Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser  
565 570 575  
5 Pro Phe Asn Asn Arg Trp Tyr Gln Met Gly Ile Val Ser Trp Gly Glu  
580 585 590  
Gly Cys Asp Arg Asp Gly Lys Tyr Gly Phe Tyr Thr His Val Phe Arg  
595 600 605  
Leu Lys Lys Trp Ile Gln Lys Val Ile Asp Gln Phe Gly Glu  
10 610 615 620

&lt;210&gt; 68

&lt;211&gt; 530

15 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Pyruvate kinase

&lt;222&gt; (1)..(530)

20 &lt;223&gt; Accession No. as of 29 August 2003: P14618

&lt;400&gt; 68

Ser Lys Pro His Ser Glu Ala Gly Thr Ala Phe Ile Gln Thr Gln Gln

1

5

10

15

211/335

Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu  
20 25 30  
Asp Ile Asp Ser Pro Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile Cys  
35 40 45  
5 Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met Ile  
50 55 60  
Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His  
65 70 75 80  
Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu Ser  
10 85 90 95  
Phe Ala Ser Asp Pro Ile Leu Tyr Arg Pro Val Ala Val Ala Leu Asp  
100 105 110  
Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr  
115 120 125  
15 Ala Glu Val Glu Leu Lys Lys Gly Ala Thr Leu Lys Ile Thr Leu Asp  
130 135 140  
Asn Ala Tyr Met Glu Lys Cys Asp Glu Asn Ile Leu Trp Leu Asp Tyr  
145 150 155 160  
Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val Asp  
20 165 170 175  
Asp Gly Leu Ile Ser Leu Gln Val Lys Gln Lys Gly Ala Asp Phe Leu  
180 185 190  
Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly Val  
195 200 205

212/335

Asn Leu Pro Gly Ala Ala Val Asp Leu Pro Ala Val Ser Glu Lys Asp  
210 215 220

Ile Gln Asp Leu Lys Phe Gly Val Glu Gln Asp Val Asp Met Val Phe  
225 230 235 240

5 Ala Ser Phe Ile Arg Lys Ala Ser Asp Val His Glu Val Arg Lys Val  
245 250 255

Leu Gly Glu Lys Gly Lys Asn Ile Lys Ile Ile Ser Lys Ile Glu Asn  
260 265 270

His Glu Gly Val Arg Arg Phe Asp Glu Ile Leu Glu Ala Ser Asp Gly  
10 275 280 285

Ile Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu Lys  
290 295 300

Val Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala Gly  
305 310 315 320

15 Lys Pro Val Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys Lys  
325 330 335

Pro Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val Leu  
340 345 350

Asp Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly Asp  
20 355 360 365

Tyr Pro Leu Glu Ala Val Arg Met Gln His Leu Ile Ala Arg Glu Ala  
370 375 380

Glu Ala Ala Ile Tyr His Leu Gln Leu Phe Glu Glu Leu Arg Arg Leu  
385 390 395 400

213/335

Ala Pro Ile Thr Ser Asp Pro Thr Glu Ala Thr Ala Val Gly Ala Val  
405 410 415

Glu Ala Ser Phe Lys Cys Cys Ser Gly Ala Ile Ile Val Leu Thr Lys  
420 425 430

5 Ser Gly Arg Ser Ala His Gln Val Ala Arg Tyr Arg Pro Arg Ala Pro  
435 440 445

Ile Ile Ala Val Thr Arg Asn Pro Gln Thr Ala Arg Gln Ala His Leu  
450 455 460

Tyr Arg Gly Ile Phe Pro Val Leu Cys Lys Asp Pro Val Gln Glu Ala  
10 465 470 475 480

Trp Ala Glu Asp Val Asp Leu Arg Val Asn Phe Ala Met Asn Val Gly  
485 490 495

Lys Ala Arg Gly Phe Phe Lys Lys Gly Asp Val Val Ile Val Leu Thr  
500 505 510

15 Gly Trp Arg Pro Gly Ser Gly Phe Thr Asn Thr Met Arg Val Val Pro  
515 520 525

Val Pro  
530

20

&lt;210&gt; 69

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

214/335

&lt;220&gt;

&lt;221&gt; Reticulocalbin 3 precursor

&lt;222&gt; (1)..(328)

&lt;223&gt; Accession No. as of 29 August 2003: Q96D15

5 &lt;400&gt; 69

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His  
 1 5 10 15  
 Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly  
 10 20 25 30  
 Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala  
 35 40 45  
 His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val  
 50 55 60  
 15 Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu  
 65 70 75 80  
 Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp  
 85 90 95  
 Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg  
 20 100 105 110  
 His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp  
 115 120 125  
 Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly  
 130 135 140



215/335

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr  
145 150 155 160  
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp  
165 170 175  
5 Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu  
180 185 190  
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr  
195 200 205  
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu  
10 210 215 220  
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala  
225 230 235 240  
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn  
245 250 255  
15 Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro  
260 265 270  
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu  
275 280 285  
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
20 290 295 300  
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
305 310 315 320  
Leu Thr Arg His His Asp Glu Leu  
325

<210> 70

<211> 469

5 <212> PRT

<213> Homo sapiens

<220>

<221> Desmin

<222> (1)..(469)

10 <223> Accession No. as of 29 August 2003: P17661

<400> 70

Ser Gln Ala Tyr Ser Ser Ser Gln Arg Val Ser Ser Tyr Arg Arg Thr

1 5 10 15

15 Phe Gly Gly Ala Pro Gly Phe Pro Leu Gly Ser Pro Leu Ser Ser Pro

20 25 30

Val Phe Pro Arg Ala Gly Phe Gly Ser Lys Gly Ser Ser Ser Ser Val

35 40 45

Thr Ser Arg Val Tyr Gln Val Ser Arg Thr Ser Gly Gly Ala Gly Gly

20 50 55 60

Leu Gly Ser Leu Arg Ala Ser Arg Leu Gly Thr Thr Arg Thr Pro Ser

65 70 75 80

Ser Tyr Gly Ala Gly Glu Leu Leu Asp Phe Ser Leu Ala Asp Ala Val

85 90 95

217/335

Asn Gln Glu Phe Leu Thr Thr Arg Thr Asn Glu Lys Val Glu Leu Gln  
100 105 110  
Glu Leu Asn Asp Arg Phe Ala Asn Tyr Ile Glu Lys Val Arg Phe Leu  
115 120 125  
5 Glu Gln Gln Asn Ala Ala Leu Ala Ala Glu Val Asn Arg Leu Lys Gly  
130 135 140  
Arg Glu Pro Thr Arg Val Ala Glu Leu Tyr Glu Glu Glu Leu Arg Glu  
145 150 155 160  
Leu Arg Arg Gln Val Glu Val Leu Thr Asn Gln Arg Ala Arg Val Asp  
10 165 170 175  
Val Glu Arg Asp Asn Leu Leu Asp Asp Leu Gln Arg Leu Lys Ala Lys  
180 185 190  
Leu Gln Glu Glu Ile Gln Leu Lys Glu Glu Ala Glu Asn Asn Leu Ala  
195 200 205  
15 Ala Phe Arg Ala Asp Val Asp Ala Ala Thr Leu Ala Arg Ile Asp Leu  
210 215 220  
Glu Arg Arg Ile Glu Ser Leu Asn Glu Glu Ile Ala Phe Leu Lys Lys  
225 230 235 240  
Val His Glu Glu Glu Ile Arg Glu Leu Gln Ala Gln Leu Gln Glu Gln  
20 245 250 255  
Gln Val Gln Val Glu Met Asp Met Ser Lys Pro Asp Leu Thr Ala Ala  
260 265 270  
Leu Arg Asp Ile Arg Ala Gln Tyr Glu Thr Ile Ala Ala Lys Asn Ile  
275 280 285

218/335

Ser Glu Ala Glu Glu Trp Tyr Lys Ser Lys Val Ser Asp Leu Thr Gln  
290 295 300

Ala Ala Asn Lys Asn Asn Asp Ala Leu Arg Gln Ala Lys Gln Glu Met  
305 310 315 320

5 Met Glu Tyr Arg His Gln Ile Gln Ser Tyr Thr Cys Glu Ile Asp Ala  
325 330 335

Leu Lys Gly Thr Asn Asp Ser Leu Met Arg Gln Met Arg Glu Leu Glu  
340 345 350

Asp Arg Phe Ala Ser Glu Ala Ser Gly Tyr Gln Asp Asn Ile Ala Arg  
10 355 360 365

Leu Glu Glu Glu Ile Arg His Leu Lys Asp Glu Met Ala Arg His Leu  
370 375 380

Arg Glu Tyr Gln Asp Leu Leu Asn Val Lys Met Ala Leu Asp Val Glu  
385 390 395 400

15 Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser Arg Ile Asn  
405 410 415

Leu Pro Ile Gln Thr Tyr Ser Ala Leu Asn Phe Arg Glu Thr Ser Pro  
420 425 430

Glu Gln Arg Gly Ser Glu Val His Thr Lys Lys Thr Val Met Ile Lys  
20 435 440 445

Thr Ile Glu Thr Arg Asp Gly Glu Val Val Ser Glu Ala Thr Gln Gln  
450 455 460

Gln His Glu Val Leu  
465

<210> 71  
<211> 417  
5 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Carboxypeptidase B precursor  
<222> (1)..(417)  
10 <223> Accession No. as of 29 August 2003: P15086  
<400> 71

Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His  
1 5 10 15  
15 His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val  
20 25 30  
Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr  
35 40 45  
Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His  
20 50 55 60  
Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu  
65 70 75 80  
Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn  
85 90 95

220/335

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr  
100 105 110

Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp  
115 120 125

5 Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val  
130 135 140

Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly  
145 150 155 160

Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His  
10 165 170 175

Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu  
180 185 190

Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp  
195 200 205

15 Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile  
210 215 220

Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His  
225 230 235 240

Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala  
20 245 250 255

Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr  
260 265 270

Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp  
275 280 285

221/335

Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His  
290 295 300  
Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu  
305 310 315 320  
5 Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys  
325 330 335  
Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala  
340 345 350  
Thr Thr Ile Tyr Pro Ala Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp  
10 355 360 365  
Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg  
370 375 380  
Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu  
385 390 395 400  
15 Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu  
405 410 415  
Tyr

20

&lt;210&gt; 72

&lt;211&gt; 419

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Carboxypeptidase A1 precursor

&lt;222&gt; (1)..(419)

&lt;223&gt; Accession No. as of 29 August 2003: P15085

5 &lt;400&gt; 72

Met Arg Gly Leu Leu Val Leu Ser Val Leu Leu Gly Ala Val Phe Gly  
1 5 10 15  
Lys Glu Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp  
10 20 25 30  
Glu Ala Gln Val Gln Lys Val Lys Glu Leu Glu Asp Leu Glu His Leu  
35 40 45  
Gln Leu Asp Phe Trp Arg Gly Pro Ala His Pro Gly Ser Pro Ile Asp  
50 55 60  
15 Val Arg Val Pro Phe Pro Ser Ile Gln Ala Val Lys Ile Phe Leu Glu  
65 70 75 80  
Ser His Gly Ile Ser Tyr Glu Thr Met Ile Glu Asp Val Gln Ser Leu  
85 90 95  
Leu Asp Glu Glu Gln Glu Gln Met Phe Ala Phe Arg Ser Arg Ala Arg  
20 100 105 110  
Ser Thr Asp Thr Phe Asn Tyr Ala Thr Tyr His Thr Leu Glu Glu Ile  
115 120 125  
Tyr Asp Phe Leu Asp Leu Leu Val Ala Glu Asn Pro His Leu Val Ser  
130 135 140



223/335

Lys Ile Gln Ile Gly Asn Thr Tyr Glu Gly Arg Pro Ile Tyr Val Leu  
 145                      150                      155                      160  
 Lys Phe Ser Thr Gly Gly Ser Lys Arg Pro Ala Ile Trp Ile Asp Thr  
                          165                      170                      175  
 5 Gly Ile His Ser Arg Glu Trp Val Thr Gln Ala Ser Gly Val Trp Phe  
                          180                      185                      190  
 Ala Lys Lys Ile Thr Gln Asp Tyr Gly Gln Asp Ala Ala Phe Thr Ala  
                          195                      200                      205  
 Ile Leu Asp Thr Leu Asp Ile Phe Leu Glu Ile Val Thr Asn Pro Asp  
 10                      210                      215                      220  
 Gly Phe Ala Phe Thr His Ser Thr Asn Arg Met Trp Arg Lys Thr Arg  
 225                      230                      235                      240  
 Ser His Thr Ala Gly Ser Leu Cys Ile Gly Val Asp Pro Asn Arg Asn  
                          245                      250                      255  
 15 Trp Asp Ala Gly Phe Gly Leu Ser Gly Ala Ser Ser Asn Pro Cys Ser  
                          260                      265                      270  
 Glu Thr Tyr His Gly Lys Phe Ala Asn Ser Glu Val Glu Val Lys Ser  
                          275                      280                      285  
 Ile Val Asp Phe Val Lys Asp His Gly Asn Ile Lys Ala Phe Ile Ser  
 20                      290                      295                      300  
 Ile His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr Lys Thr  
 305                      310                      315                      320  
 Glu Pro Val Pro Asp Gln Asp Glu Leu Asp Gln Leu Ser Lys Ala Ala  
                          325                      330                      335

224/335

Val Thr Ala Leu Ala Ser Leu Tyr Gly Thr Lys Phe Asn Tyr Gly Ser  
340 345 350  
Ile Ile Lys Ala Ile Tyr Gln Ala Ser Gly Ser Thr Ile Asp Trp Thr  
355 360 365  
5 Tyr Ser Gln Gly Ile Lys Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr  
370 375 380  
Gly Arg Tyr Gly Phe Leu Leu Pro Ala Ser Gln Ile Ile Pro Thr Ala  
385 390 395 400  
Lys Glu Thr Trp Leu Ala Leu Leu Thr Ile Met Glu His Thr Leu Asn  
10 405 410 415  
His Pro Tyr

15 &lt;210&gt; 73

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

20 &lt;221&gt; Colligin 2

&lt;222&gt; (1)..(418)

&lt;223&gt; Accession No. as of 29 August 2003: P50454

&lt;400&gt; 73

225/335

Met Arg Ser Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala  
1 5 10 15  
Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr  
20 25 30  
5 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala  
35 40 45  
Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val  
50 55 60  
Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu  
10 65 70 75 80  
Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val  
85 90 95  
Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly  
100 105 110  
15 Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp  
115 120 125  
Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp  
130 135 140  
Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys  
20 145 150 155 160  
Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp  
165 170 175  
Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val  
180 185 190

226/335

Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro  
195 200 205

His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe  
210 215 220

5 Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr  
225 230 235 240

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val  
245 250 255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro  
10 260 265 270

His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu  
275 280 285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile  
290 295 300

15 Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His  
305 310 315 320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp  
325 330 335

Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe  
20 340 345 350

His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln  
355 360 365

Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala  
370 375 380

227/335

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu

385                      390                      395                      400

Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp

405                      410                      415

5 Glu Leu

<210> 74

10 <211> 263

<212> PRT

<213> Homo sapiens

<220>

<221> Chymotrypsinogen B precursor

15 <222> (1)..(263)

<223> Accession No. as of 29 August 2003: P17538

<400> 74

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr

20 1                      5                      10                      15

Phe Gly Cys Gly Val Pro Ala Ile His Pro Val Leu Ser Gly Leu Ser

20                      25                      30

Arg Ile Val Asn Gly Glu Asp Ala Val Pro Gly Ser Trp Pro Trp Gln

35                      40                      45

Val Ser Leu Gln Asp Lys Thr Gly Phe His Phe Cys Gly Gly Ser Leu  
50 55 60  
Ile Ser Glu Asp Trp Val Val Thr Ala Ala His Cys Gly Val Arg Thr  
65 70 75 80  
5 Ser Asp Val Val Val Ala Gly Glu Phe Asp Gln Gly Ser Asp Glu Glu  
85 90 95  
Asn Ile Gln Val Leu Lys Ile Ala Lys Val Phe Lys Asn Pro Lys Phe  
100 105 110  
Ser Ile Leu Thr Val Asn Asn Asp Ile Thr Leu Leu Lys Leu Ala Thr  
10 115 120 125  
Pro Ala Arg Phe Ser Gln Thr Val Ser Ala Val Cys Leu Pro Ser Ala  
130 135 140  
Asp Asp Asp Phe Pro Ala Gly Thr Leu Cys Ala Thr Thr Gly Trp Gly  
145 150 155 160  
15 Lys Thr Lys Tyr Asn Ala Asn Lys Thr Pro Asp Lys Leu Gln Gln Ala  
165 170 175  
Ala Leu Pro Leu Leu Ser Asn Ala Glu Cys Lys Lys Ser Trp Gly Arg  
180 185 190  
Arg Ile Thr Asp Val Met Ile Cys Ala Gly Ala Ser Gly Val Ser Ser  
20 195 200 205  
Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Asp Gly Ala  
210 215 220  
Trp Thr Leu Val Gly Ile Val Ser Trp Gly Ser Asp Thr Cys Ser Thr  
225 230 235 240

229/335

Ser Ser Pro Gly Val Tyr Ala Arg Val Thr Lys Leu Ile Pro Trp Val

245

250

255

Gln Lys Ile Leu Ala Ala Asn

260

5

&lt;210&gt; 75

&lt;211&gt; 247

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Trypsin I precursor

&lt;222&gt; (1) .. (247)

&lt;223&gt; Accession No. as of 29 August 2003: P07477

15 &lt;400&gt; 75

Met Asn Pro Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Leu Ala Ala

1

5

10

15

Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Glu Glu

20

20

25

30

Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys

35

40

45

Gly Gly Ser Leu Ile Asn Glu Gln Trp Val Val Ser Ala Gly His Cys

50

55

60

230/335

Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val  
65 70 75 80  
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His  
85 90 95  
5 Pro Gln Tyr Asp Arg Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys  
100 105 110  
Leu Ser Ser Arg Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu  
115 120 125  
Pro Thr Ala Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp  
10 130 135 140  
Gly Asn Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys  
145 150 155 160  
Leu Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro  
165 170 175  
15 Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly  
180 185 190  
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly  
195 200 205  
Gln Leu Gln Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Lys Asn  
20 210 215 220  
Lys Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Lys Trp Ile Lys  
225 230 235 240  
Asn Thr Ile Ala Ala Asn Ser

245



<210> 76  
<211> 247  
5 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Trypsin II precursor  
<222> (1)..(247)  
10 <223> Accession No. as of 29 August 2003: P07478  
<400> 76  
  
Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala Ala  
1 5 10 15  
15 Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ile Cys Glu Glu  
20 25 30  
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys  
35 40 45  
Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Gly His Cys  
20 50 55 60  
Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val  
65 70 75 80  
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His  
85 90 95

232/335

Pro Lys Tyr Asn Ser Arg Thr Leu Asp Asn Asp Ile Leu Leu Ile Lys  
100 105 110

Leu Ser Ser Pro Ala Val Ile Asn Ser Arg Val Ser Ala Ile Ser Leu  
115 120 125

5 Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Ser Leu Ile Ser Gly Trp  
130 135 140

Gly Asn Thr Leu Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys  
145 150 155 160

Leu Asp Ala Pro Val Leu Ser Gln Ala Glu Cys Glu Ala Ser Tyr Pro  
10 165 170 175

Gly Lys Ile Thr Asn Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly  
180 185 190

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Ser Asn Gly  
195 200 205

15 Glu Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Asn  
210 215 220

Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys  
225 230 235 240

Asp Thr Ile Ala Ala Asn Ser  
20 245

&lt;210&gt; 77

&lt;211&gt; 379

233/335

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Leukocyte elastase inhibitor (LEI)

5 &lt;222&gt; (1)..(379)

&lt;223&gt; Accession No. as of 29 August 2003: P30740

&lt;400&gt; 77

Met Glu Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe  
10 1 5 10 15  
Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro  
20 25 30  
Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly  
35 40 45  
15 Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu  
50 55 60  
Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg  
65 70 75 80  
Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys  
20 85 90 95  
Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr  
100 105 110  
Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala  
115 120 125

234/335

Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile  
130 135 140

Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val  
145 150 155 160

5 Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met  
165 170 175

Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg  
180 185 190

Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr  
10 195 200 205

Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu  
210 215 220

Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser  
225 230 235 240

15 Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His  
245 250 255

Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser  
260 265 270

Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu  
20 275 280 285

Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu  
290 295 300

Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His  
305 310 315 320

235/335

Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala

325

330

335

Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe

340

345

350

5 Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly

355

360

365

Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro

370

375

10

&lt;210&gt; 78

&lt;211&gt; 573

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15 &lt;220&gt;

&lt;221&gt; Hsp60

&lt;222&gt; (1)..(573)

&lt;223&gt; Accession No. as of 29 August 2003: P10809

&lt;400&gt; 78

20

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg

1

5

10

15

Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe

20

25

30

236/335

Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
 35 40 45  
 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile  
 50 55 60  
 5 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val  
 65 70 75 80  
 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys  
 85 90 95  
 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly  
 10 100 105 110  
 Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe  
 115 120 125  
 Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val  
 130 135 140  
 15 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys  
 145 150 155 160  
 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala  
 165 170 175  
 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys  
 20 180 185 190  
 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn  
 195 200 205  
 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile  
 210 215 220

237/335

Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln  
225 230 235 240  
Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser  
245 250 255  
5 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val  
260 265 270  
Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu  
275 280 285  
Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly  
10 290 295 300  
Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr  
305 310 315 320  
Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp  
325 330 335  
15 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys  
340 345 350  
Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu  
355 360 365  
Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu  
20 370 375 380  
Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly  
385 390 395 400  
Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu  
405 410 415

238/335

Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val  
420 425 430

Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile  
435 440 445

5 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly  
450 455 460

Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala  
465 470 475 480

Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln  
10 485 490 495

Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn  
500 505 510

Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala  
515 520 525

15 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val  
530 535 540

Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala  
545 550 555 560

Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe  
20 565 570

&lt;210&gt; 79

&lt;211&gt; 803



<212> PRT

<213> Homo sapiens

<220>

<221> Endoplasmin precursor (GRP94)

5 <222> (1)..(803)

<223> Accession No. as of 29 August 2003: P14625

<400> 79

Met Arg Ala Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe  
10 1 5 10 15  
Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu  
20 25 30  
Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val  
35 40 45  
15 Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser  
50 55 60  
Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala  
65 70 75 80  
Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn  
20 85 90 95  
Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu  
100 105 110  
Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly  
115 120 125

240/335

Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu  
130 135 140  
Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val  
145 150 155 160  
5 Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn  
165 170 175  
Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile  
180 185 190  
Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys  
10 195 200 205  
Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu  
210 215 220  
Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr  
225 230 235 240  
15 Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser  
245 250 255  
Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser  
260 265 270  
Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr  
20 275 280 285  
Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu  
290 295 300  
Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Glu Lys Lys  
305 310 315 320

241/335

Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met  
325 330 335

Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu  
340 345 350

5 Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp  
355 360 365

Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys  
370 375 380

Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp Glu  
10 385 390 395 400

Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val  
405 410 415

Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn Phe  
420 425 430

15 Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg  
435 440 445

Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu  
450 455 460

Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr  
20 465 470 475 480

Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val  
485 490 495

Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg Phe  
500 505 510

242/335

Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val  
515 520 525

Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser  
530 535 540

5 Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys  
545 550 555 560

Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys  
565 570 575

Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala  
10 580 585 590

Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg  
595 600 605

Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp  
610 615 620

15 Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu  
625 630 635 640

Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly  
645 650 655

Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp  
20 660 665 670

Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn  
675 680 685

Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp  
690 695 700

243/335

Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu Thr  
705 710 715 720  
Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly  
725 730 735  
5 Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro Asp  
740 745 750  
Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala Glu  
755 760 765  
Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp Val  
10 770 775 780  
Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu Lys  
785 790 795 800  
Asp Glu Leu

15

&lt;210&gt; 80

&lt;211&gt; 261

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)

&lt;222&gt; (1)..(261)

&lt;223&gt; Accession No. as of 29 August 2003: P30040

244/335

&lt;400&gt; 80

Met Ala Ala Ala Val Pro Arg Ala Ala Phe Leu Ser Pro Leu Leu Pro  
1 5 10 15  
5 Leu Leu Leu Gly Phe Leu Leu Leu Ser Ala Pro His Gly Gly Ser Gly  
20 25 30  
Leu His Thr Lys Gly Ala Leu Pro Leu Asp Thr Val Thr Phe Tyr Lys  
35 40 45  
Val Ile Pro Lys Ser Lys Phe Val Leu Val Lys Phe Asp Thr Gln Tyr  
10 50 55 60  
Pro Tyr Gly Glu Lys Gln Asp Glu Phe Lys Arg Leu Ala Glu Asn Ser  
65 70 75 80  
Ala Ser Ser Asp Asp Leu Leu Val Ala Glu Val Gly Ile Ser Asp Tyr  
85 90 95  
15 Gly Asp Lys Leu Asn Met Glu Leu Ser Glu Lys Tyr Lys Leu Asp Lys  
100 105 110  
Glu Ser Tyr Pro Val Phe Tyr Leu Phe Arg Asp Gly Asp Phe Glu Asn  
115 120 125  
Pro Val Pro Tyr Thr Gly Ala Val Lys Val Gly Ala Ile Gln Arg Trp  
20 130 135 140  
Leu Lys Gly Gln Gly Val Tyr Leu Gly Met Pro Gly Cys Leu Pro Val  
145 150 155 160  
Tyr Asp Ala Leu Ala Gly Glu Phe Ile Arg Ala Ser Gly Val Glu Ala  
165 170 175

245/335

Arg Gln Ala Leu Leu Lys Gln Gly Gln Asp Asn Leu Ser Ser Val Lys  
180 185 190  
Glu Thr Gln Lys Lys Trp Ala Glu Gln Tyr Leu Lys Ile Met Gly Lys  
195 200 205  
5 Ile Leu Asp Gln Gly Glu Asp Phe Pro Ala Ser Glu Met Thr Arg Ile  
210 215 220  
Ala Arg Leu Ile Glu Lys Asn Lys Met Ser Asp Gly Lys Lys Glu Glu  
225 230 235 240  
Leu Gln Lys Ser Leu Asn Ile Leu Thr Ala Phe Gln Lys Lys Gly Ala  
10 245 250 255  
Glu Lys Glu Glu Leu  
260

15 &lt;210&gt; 81

&lt;211&gt; 525

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

20 &lt;221&gt; Protein disulfide isomerase A2 precursor

&lt;222&gt; (1)..(525)

&lt;223&gt; Accession No. as of 29 August 2003: Q13087

&lt;400&gt; 81

246/335

Met Ser Arg Gln Leu Leu Pro Val Leu Leu Leu Leu Leu Leu Arg Ala  
1 5 10 15  
Ser Cys Pro Trp Gly Gln Glu Gln Gly Ala Arg Ser Pro Ser Glu Glu  
20 25 30  
5 Pro Pro Glu Glu Glu Ile Pro Lys Glu Asp Gly Ile Leu Val Leu Ser  
35 40 45  
Arg His Thr Leu Gly Leu Ala Leu Arg Glu His Pro Ala Leu Leu Val  
50 55 60  
Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu  
10 65 70 75 80  
Tyr Ser Lys Ala Ala Ala Val Leu Ala Ala Glu Ser Met Val Val Thr  
85 90 95  
Leu Ala Lys Val Asp Gly Pro Ala Gln Arg Glu Leu Ala Glu Glu Phe  
100 105 110  
15 Gly Val Thr Glu Tyr Pro Thr Leu Lys Phe Phe Arg Asn Gly Asn Arg  
115 120 125  
Thr His Pro Glu Glu Tyr Thr Gly Pro Arg Asp Ala Glu Gly Ile Ala  
130 135 140  
Glu Trp Leu Arg Arg Arg Val Gly Pro Ser Ala Met Arg Leu Glu Asp  
20 145 150 155 160  
Glu Ala Ala Ala Gln Ala Leu Ile Gly Gly Arg Asp Leu Val Val Ile  
165 170 175  
Gly Phe Phe Gln Asp Leu Gln Asp Glu Asp Val Ala Thr Phe Leu Ala  
180 185 190



247/335

Leu Ala Gln Asp Ala Leu Asp Met Thr Phe Gly Leu Thr Asp Arg Pro  
195 200 205

Arg Leu Phe Gln Gln Phe Gly Leu Thr Lys Asp Thr Val Val Leu Phe  
210 215 220

5 Lys Lys Phe Asp Glu Gly Arg Ala Asp Phe Pro Val Asp Glu Glu Leu  
225 230 235 240

Gly Leu Asp Leu Gly Asp Leu Ser Arg Phe Leu Val Thr His Ser Met  
245 250 255

Arg Leu Val Thr Glu Phe Asn Ser Gln Thr Ser Ala Lys Ile Phe Ala  
10 260 265 270

Ala Arg Ile Leu Asn His Leu Leu Leu Phe Val Asn Gln Thr Leu Ala  
275 280 285

Ala His Arg Glu Leu Leu Ala Gly Phe Gly Glu Ala Ala Pro Arg Phe  
290 295 300

15 Arg Gly Gln Val Leu Phe Val Val Val Asp Val Ala Ala Asp Asn Glu  
305 310 315 320

His Val Leu Gln Tyr Phe Gly Leu Lys Ala Glu Ala Ala Pro Thr Leu  
325 330 335

Arg Leu Val Asn Leu Glu Thr Thr Lys Lys Tyr Ala Pro Val Asp Gly  
20 340 345 350

Gly Pro Val Thr Ala Ala Ser Ile Thr Ala Phe Cys His Ala Val Leu  
355 360 365

Asn Gly Gln Val Lys Pro Tyr Leu Leu Ser Gln Glu Ile Pro Pro Asp  
370 375 380

248/335

Trp Asp Gln Arg Pro Val Lys Thr Leu Val Gly Lys Asn Phe Glu Gln  
385 390 395 400  
Val Ala Phe Asp Glu Thr Lys Asn Val Phe Val Lys Phe Tyr Ala Pro  
405 410 415  
5 Trp Cys Thr His Cys Lys Glu Met Ala Pro Ala Trp Glu Ala Leu Ala  
420 425 430  
Glu Lys Tyr Gln Asp His Glu Asp Ile Ile Ile Ala Glu Leu Asp Ala  
435 440 445  
Thr Ala Asn Glu Leu Asp Ala Phe Ala Val His Gly Phe Pro Thr Leu  
10 450 455 460  
Lys Tyr Phe Pro Ala Gly Pro Gly Arg Lys Val Ile Glu Tyr Lys Ser  
465 470 475 480  
Thr Arg Asp Leu Glu Thr Phe Ser Lys Phe Leu Asp Asn Gly Gly Val  
485 490 495  
15 Leu Pro Thr Glu Glu Pro Pro Glu Glu Pro Ala Ala Pro Phe Pro Glu  
500 505 510  
Pro Pro Ala Asn Ser Thr Met Gly Ser Lys Glu Glu Leu  
515 520 525  
20  
<210> 82  
<211> 505  
<212> PRT  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; Protein disulfide isomerase A3 precursor

&lt;222&gt; (1)..(505)

&lt;223&gt; Accession No. as of 29 August 2003: P30101

5 &lt;400&gt; 82

Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu  
1 5 10 15  
Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp  
10 20 25 30  
Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met  
35 40 45  
Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala  
50 55 60  
15 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu  
65 70 75 80  
Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly  
85 90 95  
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala  
20 100 105 110  
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu  
115 120 125  
Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu  
130 135 140

250/335

Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe  
145 150 155 160  
Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser  
165 170 175  
5 Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu  
180 185 190  
Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro  
195 200 205  
Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu  
10 210 215 220  
Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile  
225 230 235 240  
Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln  
245 250 255  
15 Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn  
260 265 270  
Ala Lys Gly Ser Asn Tyr Trp Arg Asn Arg Val Met Met Val Ala Lys  
275 280 285  
Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg  
20 290 295 300  
Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala  
305 310 315 320  
Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe  
325 330 335

251/335

Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe  
340 345 350  
Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu  
355 360 365  
5 Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu  
370 375 380  
Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu  
385 390 395 400  
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr  
10 405 410 415  
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala  
420 425 430  
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg  
435 440 445  
15 Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro  
450 455 460  
Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu  
465 470 475 480  
Gln Arg Glu Ala Thr Asn Pro Pro Val Ile Gln Glu Glu Lys Pro Lys  
20 485 490 495  
Lys Lys Lys Lys Ala Gln Glu Asp Leu  
500 505

252/335

&lt;210&gt; 83

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; Alcohol dehydrogenase beta chain

&lt;222&gt; (1)..(374)

&lt;223&gt; Accession No. as of 29 August 2003: P00325

&lt;400&gt; 83

10

Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu

1 5 10 15

Val Lys Lys Pro Phe Ser Ile Glu Asp Val Glu Val Ala Pro Pro Lys

20 25 30

15 Ala Tyr Glu Val Arg Ile Lys Met Val Ala Val Gly Ile Cys Arg Thr

35 40 45

Asp Asp His Val Val Ser Gly Asn Leu Val Thr Pro Leu Pro Val Ile

50 55 60

Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly Glu Gly Val

20 65 70 75 80

Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro Gln

85 90 95

Cys Gly Lys Cys Arg Val Cys Lys Asn Pro Glu Ser Asn Tyr Cys Leu

100 105 110

253/335

Lys Asn Asp Leu Gly Asn Pro Arg Gly Thr Leu Gln Asp Gly Thr Arg  
115 120 125

Arg Phe Thr Cys Arg Gly Lys Pro Ile His His Phe Leu Gly Thr Ser  
130 135 140

5 Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Asn Ala Val Ala Lys Ile  
145 150 155 160

Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys Gly Phe  
165 170 175

Ser Thr Gly Tyr Gly Ser Ala Val Asn Val Ala Lys Val Thr Pro Gly  
10 180 185 190

Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Ala Val  
195 200 205

Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp Ile  
210 215 220

15 Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu Cys  
225 230 235 240

Ile Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Lys Glu  
245 250 255

Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg Leu  
20 260 265 270

Asp Thr Met Met Ala Ser Leu Leu Cys Cys His Glu Ala Cys Gly Thr  
275 280 285

Ser Val Ile Val Gly Val Pro Pro Ala Ser Gln Asn Leu Ser Ile Asn  
290 295 300

254/335

Pro Met Leu Leu Leu Thr Gly Arg Thr Trp Lys Gly Ala Val Tyr Gly  
305 310 315 320  
Gly Phe Lys Ser Lys Glu Gly Ile Pro Lys Leu Val Ala Asp Phe Met  
325 330 335  
5 Ala Lys Lys Phe Ser Leu Asp Ala Leu Ile Thr His Val Leu Pro Phe  
340 345 350  
Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu His Ser Gly Lys Ser Ile  
355 360 365  
Arg Thr Val Leu Thr Phe  
10 370

&lt;210&gt; 84

&lt;211&gt; 241

15 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Glutathione transferase omega 1

&lt;222&gt; (1)..(241)

20 &lt;223&gt; Accession No. as of 29 August 2003: P78417

&lt;400&gt; 84

Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro

1

5

10

15



255/335

Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys  
 20 25 30  
 Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg  
 35 40 45  
 5 His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe  
 50 55 60  
 Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly  
 65 70 75 80  
 Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala  
 10 85 90 95  
 Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys  
 100 105 110  
 Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly  
 115 120 125  
 15 Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu  
 130 135 140  
 Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys  
 145 150 155 160  
 Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu  
 20 165 170 175  
 Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys  
 180 185 190  
 Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu  
 195 200 205

256/335

Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly

210

215

220

Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly

225

230

235

240

5 Leu

&lt;210&gt; 85

10 &lt;211&gt; 999

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; 150 kDa oxygen-regulated protein precursor (Orp150)

15 &lt;222&gt; (1)..(999)

&lt;223&gt; Accession No. as of 29 August 2003: Q9Y4L1

&lt;400&gt; 85

Met Ala Asp Lys Val Arg Arg Gln Arg Pro Arg Arg Arg Val Cys Trp

20 1

5

10

15

Ala Leu Val Ala Val Leu Leu Ala Asp Leu Leu Ala Leu Ser Asp Thr

20

25

30

Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met Lys Val Ala

35

40

45

257/335

Ile Val Lys Pro Gly Val Pro Met Glu Ile Val Leu Asn Lys Glu Ser  
50 55 60  
Arg Arg Lys Thr Pro Val Ile Val Thr Leu Lys Glu Asn Glu Arg Phe  
65 70 75 80  
5 Phe Gly Asp Ser Ala Ala Ser Met Ala Ile Lys Asn Pro Lys Ala Thr  
85 90 95  
Leu Arg Tyr Phe Gln His Leu Leu Gly Lys Gln Ala Asp Asn Pro His  
100 105 110  
Val Ala Leu Tyr Gln Ala Arg Phe Pro Glu His Glu Leu Thr Phe Asp  
10 115 120 125  
Pro Gln Arg Gln Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe  
130 135 140  
Ser Pro Glu Glu Val Leu Gly Met Val Leu Asn Tyr Ser Arg Ser Leu  
145 150 155 160  
15 Ala Glu Asp Phe Ala Glu Gln Pro Ile Lys Asp Ala Val Ile Thr Val  
165 170 175  
Pro Val Phe Phe Asn Gln Ala Glu Arg Arg Ala Val Leu Gln Ala Ala  
180 185 190  
Arg Met Ala Gly Leu Lys Val Leu Gln Leu Ile Asn Asp Asn Thr Ala  
20 195 200 205  
Thr Ala Leu Ser Tyr Gly Val Phe Arg Arg Lys Asp Ile Asn Thr Thr  
210 215 220  
Ala Gln Asn Ile Met Phe Tyr Asp Met Gly Ser Gly Ser Thr Val Cys  
225 230 235 240

258/335

Thr Ile Val Thr Tyr Gln Met Val Lys Thr Lys Glu Ala Gly Met Gln  
245 250 255

Pro Gln Leu Gln Ile Arg Gly Val Gly Phe Asp Arg Thr Leu Gly Gly  
260 265 270

5 Leu Glu Met Glu Leu Arg Leu Arg Glu Arg Leu Ala Gly Leu Phe Asn  
275 280 285

Glu Gln Arg Lys Gly Gln Arg Ala Lys Asp Val Arg Glu Asn Pro Arg  
290 295 300

Ala Met Ala Lys Leu Leu Arg Glu Ala Asn Arg Leu Lys Thr Val Leu  
10 305 310 315 320

Ser Ala Asn Ala Asp His Met Ala Gln Ile Glu Gly Leu Met Asp Asp  
325 330 335

Val Asp Phe Lys Ala Lys Val Thr Arg Val Glu Phe Glu Glu Leu Cys  
340 345 350

15 Ala Asp Leu Phe Glu Arg Val Pro Gly Pro Val Gln Gln Ala Leu Gln  
355 360 365

Ser Ala Glu Met Ser Leu Asp Glu Ile Glu Gln Val Ile Leu Val Gly  
370 375 380

Gly Ala Thr Arg Val Pro Arg Val Gln Glu Val Leu Leu Lys Ala Val  
20 385 390 395 400

Gly Lys Glu Glu Leu Gly Lys Asn Ile Asn Ala Asp Glu Ala Ala Ala  
405 410 415

Met Gly Ala Val Tyr Gln Ala Ala Ala Leu Ser Lys Ala Phe Lys Val  
420 425 430

259/335

Lys Pro Phe Val Val Arg Asp Ala Val Val Tyr Pro Ile Leu Val Glu  
435 440 445

Phe Thr Arg Glu Val Glu Glu Glu Pro Gly Ile His Ser Leu Lys His  
450 455 460

5 Asn Lys Arg Val Leu Phe Ser Arg Met Gly Pro Tyr Pro Gln Arg Lys  
465 470 475 480

Val Ile Thr Phe Asn Arg Tyr Ser His Asp Phe Asn Phe His Ile Asn  
485 490 495

Tyr Gly Asp Leu Gly Phe Leu Gly Pro Glu Asp Leu Arg Val Phe Gly  
10 500 505 510

Ser Gln Asn Leu Thr Thr Val Lys Leu Lys Gly Val Gly Asp Ser Phe  
515 520 525

Lys Lys Tyr Pro Asp Tyr Glu Ser Lys Gly Ile Lys Ala His Phe Asn  
530 535 540

15 Leu Asp Glu Ser Gly Val Leu Ser Leu Asp Arg Val Glu Ser Val Phe  
545 550 555 560

Glu Thr Leu Val Glu Asp Ser Ala Glu Glu Glu Ser Thr Leu Thr Lys  
565 570 575

Leu Gly Asn Thr Ile Ser Ser Leu Phe Gly Gly Gly Thr Thr Pro Asp  
20 580 585 590

Ala Lys Glu Asn Gly Thr Asp Thr Val Gln Glu Glu Glu Glu Ser Pro  
595 600 605

Ala Glu Gly Ser Lys Asp Glu Pro Gly Glu Gln Val Glu Leu Lys Glu  
610 615 620

260/335

Glu Ala Glu Ala Pro Val Glu Asp Gly Ser Gln Pro Pro Pro Pro Glu  
625 630 635 640  
Pro Lys Gly Asp Ala Thr Pro Glu Gly Glu Lys Ala Thr Glu Lys Glu  
645 650 655  
5 Asn Gly Asp Lys Ser Glu Ala Gln Lys Pro Ser Glu Lys Ala Glu Ala  
660 665 670  
Gly Pro Glu Gly Val Ala Pro Ala Pro Glu Gly Glu Lys Lys Gln Lys  
675 680 685  
Pro Ala Arg Lys Arg Arg Met Val Glu Glu Ile Gly Val Glu Leu Val  
10 690 695 700  
Val Leu Asp Leu Pro Asp Leu Pro Glu Asp Lys Leu Ala Gln Ser Val  
705 710 715 720  
Gln Lys Leu Gln Asp Leu Thr Leu Arg Asp Leu Glu Lys Gln Glu Arg  
725 730 735  
15 Glu Lys Ala Ala Asn Ser Leu Glu Ala Phe Ile Phe Glu Thr Gln Asp  
740 745 750  
Lys Leu Tyr Gln Pro Glu Tyr Gln Glu Val Ser Thr Glu Glu Gln Arg  
755 760 765  
Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp  
20 770 775 780  
Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu  
785 790 795 800  
Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys  
805 810 815

261/335

Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Leu Asn His Ser  
820 825 830

Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile  
835 840 845

5 Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr  
850 855 860

Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala  
865 870 875 880

Thr Glu Lys Pro Val Leu Leu Ser Lys Asp Ile Glu Ala Lys Met Met  
10 885 890 895

Ala Leu Asp Arg Glu Val Gln Tyr Leu Leu Asn Lys Ala Lys Phe Thr  
900 905 910

Lys Pro Arg Pro Arg Pro Lys Asp Lys Asn Gly Thr Arg Ala Glu Pro  
915 920 925

15 Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Glu Lys Val Ile Pro Pro  
930 935 940

Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val  
945 950 955 960

Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly  
20 965 970 975

Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg  
980 985 990

Pro Leu Lys Asn Asp Glu Leu  
995

<210> 86  
<211> 271  
5 <212> PRT  
<213> Homo sapiens  
<220>  
<221> Peroxiredoxin 4  
<222> (1)..(271)  
10 <223> Accession No. as of 29 August 2003: Q13162  
<400> 86

Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg  
1 5 10 15  
15 His Arg Arg Leu Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala  
20 25 30  
Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu  
35 40 45  
Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala  
20 50 55 60  
Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys  
65 70 75 80  
Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly  
85 90 95



263/335

Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val  
100 105 110  
Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile  
115 120 125  
5 Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu  
130 135 140  
Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile  
145 150 155 160  
Asn Thr Pro Arg Arg Gln Gly Gly Leu Gly Pro Ile Arg Ile Pro Leu  
10 165 170 175  
Leu Ser Asp Leu Thr His Gln Ile Ser Lys Asp Tyr Gly Val Tyr Leu  
180 185 190  
Glu Asp Ser Gly His Thr Leu Arg Gly Leu Phe Ile Ile Asp Asp Lys  
195 200 205  
15 Gly Ile Leu Arg Gln Ile Thr Leu Asn Asp Leu Pro Val Gly Arg Ser  
210 215 220  
Val Asp Glu Thr Leu Arg Leu Val Gln Ala Phe Gln Tyr Thr Asp Lys  
225 230 235 240  
His Gly Glu Val Cys Pro Ala Gly Trp Lys Pro Gly Ser Glu Thr Ile  
20 245 250 255  
Ile Pro Asp Pro Ala Gly Lys Leu Lys Tyr Phe Asp Lys Leu Asn  
260 265 270

264/335

&lt;210&gt; 87

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; MAWD binding protein

&lt;222&gt; (1)..(288)

&lt;223&gt; Accession No. as of 29 August 2003: P30039

&lt;400&gt; 87

10

Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala Arg Ala Phe

1

5

10

15

Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu Leu Asp Glu

20

25

30

15 Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser Glu Thr Ala

35

40

45

Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln Ser Ser Cys

50

55

60

Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro Leu Cys Gly

20 65

70

75

80

His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys Ile Lys Asn

85

90

95

Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu Leu Arg Ala

100

105

110

265/335

Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu Tyr Pro Ala  
115 120 125

His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys Thr Ala Ile  
130 135 140

5 Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp Thr Gln Lys  
145 150 155 160

Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe Leu Glu Asn  
165 170 175

Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn Thr Gly Lys  
10 180 185 190

Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly Gly Gln Thr  
195 200 205

Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp Val Gly Val  
210 215 220

15 Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu Ser Ser Tyr  
225 230 235 240

Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe Gln Cys Ser  
245 250 255

His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp Gly Arg Val  
20 260 265 270

Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr Leu Thr Ala  
275 280 285

<210> 88

<211> 511

<212> PRT

<213> Homo sapiens

5 <220>

<221> Alpha-amylase 2B precursor

<222> (1)..(511)

<223> Accession No. as of 29 August 2003: P19961

<400> 88

10

Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln

1 5 10 15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe

20 25 30

15 Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala

35 40 45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val

50 55 60

Ala Ile His Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val

20 65 70 75 80

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn

85 90 95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala

100 105 110

267/335

Val Ile Asn His Met Ser Gly Asn Ala Val Ser Ala Gly Thr Ser Ser  
115 120 125

Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val  
130 135 140

5 Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser  
145 150 155 160

Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg  
165 170 175

Leu Val Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser  
10 180 185 190

Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly  
195 200 205

Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala  
210 215 220

15 Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly  
225 230 235 240

Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro  
245 250 255

Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys  
20 260 265 270

Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys  
275 280 285

Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Met Pro Ser  
290 295 300

268/335

Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His  
305 310 315 320  
Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr  
325 330 335  
5 Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg  
340 345 350  
Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp  
355 360 365  
Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu  
10 370 375 380  
Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu  
385 390 395 400  
His Arg Trp Arg Gln Ile Arg Asn Met Val Asn Phe Arg Asn Val Val  
405 410 415  
15 Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val  
420 425 430  
Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp  
435 440 445  
Trp Thr Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr  
20 450 455 460  
Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile  
465 470 475 480  
Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn  
485 490 495

Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu

500

505

510

5 <210> 89

<211> 511

<212> PRT

<213> Homo sapiens

<220>

10 <221> Alpha-amylase, pancreatic precursor

<222> (1)..(511)

<223> Accession No. as of 29 August 2003: P04746

<400> 89

15 Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln

1 5 10 15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe

20 25 30

Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala

20 35 40 45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val

50 55 60

Ala Ile Tyr Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val

65 70 75 80

270/335

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn  
85 90 95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala  
100 105 110

5 Val Ile Asn His Met Cys Gly Asn Ala Val Ser Ala Gly Thr Ser Ser  
115 120 125

Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val  
130 135 140

Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser  
10 145 150 155 160

Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg  
165 170 175

Leu Thr Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser  
180 185 190

15 Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly  
195 200 205

Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala  
210 215 220

Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly  
20 225 230 235 240

Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro  
245 250 255

Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys  
260 265 270



271/335

Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys  
275 280 285

Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Val Pro Ser  
290 295 300

5 Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His  
305 310 315 320

Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr  
325 330 335

Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg  
10 340 345 350

Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp  
355 360 365

Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu  
370 375 380

15 Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu  
385 390 395 400

His Arg Trp Arg Gln Ile Arg Asn Met Val Ile Phe Arg Asn Val Val  
405 410 415

Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val  
20 420 425 430

Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp  
435 440 445

Trp Ser Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr  
450 455 460

272/335

Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile  
465 470 475 480  
Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn  
485 490 495  
5 Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu  
500 505 510

<210> 90  
10 <211> 553  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> ATP synthase alpha chain  
15 <222> (1)..(553)  
<223> Accession No. as of 29 August 2003: P25705  
<400> 90

Met Leu Ser Val Arg Val Ala Ala Ala Val Val Arg Ala Leu Pro Arg  
20 1 5 10 15  
Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala  
20 25 30  
Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr  
35 40 45

273/335

Ala Glu Met Ser Ser Ile Leu Glu Glu Arg Ile Leu Gly Ala Asp Thr  
50 55 60  
Ser Val Asp Leu Glu Glu Thr Gly Arg Val Leu Ser Ile Gly Asp Gly  
65 70 75 80  
5 Ile Ala Arg Val His Gly Leu Arg Asn Val Gln Ala Glu Glu Met Val  
85 90 95  
Glu Phe Ser Ser Gly Leu Lys Gly Met Ser Leu Asn Leu Glu Pro Asp  
100 105 110  
Asn Val Gly Val Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly  
10 115 120 125  
Asp Ile Val Lys Arg Thr Gly Ala Ile Val Asp Val Pro Val Gly Glu  
130 135 140  
Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly  
145 150 155 160  
15 Lys Gly Pro Ile Gly Ser Lys Thr Arg Arg Arg Val Gly Leu Lys Ala  
165 170 175  
Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly  
180 185 190  
Ile Lys Ala Val Asp Ser Leu Val Pro Ile Gly Arg Gly Gln Arg Glu  
20 195 200 205  
Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp  
210 215 220  
Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys  
225 230 235 240

274/335

Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val  
245 250 255

Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr  
260 265 270

5 Ile Val Val Ser Ala Thr Ala Ser Asp Ala Ala Pro Leu Gln Tyr Leu  
275 280 285

Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly  
290 295 300

Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala  
10 305 310 315 320

Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala  
325 330 335

Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala  
340 345 350

15 Ala Lys Met Asn Asp Ala Phe Gly Gly Gly Ser Leu Thr Ala Leu Pro  
355 360 365

Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn  
370 375 380

Val Ile Ser Ile Thr Asp Gly Gln Ile Phe Leu Glu Thr Glu Leu Phe  
20 385 390 395 400

Tyr Lys Gly Ile Arg Pro Ala Ile Asn Val Gly Leu Ser Val Ser Arg  
405 410 415

Val Gly Ser Ala Ala Gln Thr Arg Ala Met Lys Gln Val Ala Gly Thr  
420 425 430

275/335

Met Lys Leu Glu Leu Ala Gln Tyr Arg Glu Val Ala Ala Phe Ala Gln  
435 440 445  
Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Gln Leu Leu Ser Arg Gly  
450 455 460  
5 Val Arg Leu Thr Glu Leu Leu Lys Gln Gly Gln Tyr Ser Pro Met Ala  
465 470 475 480  
Ile Glu Glu Gln Val Ala Val Ile Tyr Ala Gly Val Arg Gly Tyr Leu  
485 490 495  
Asp Lys Leu Glu Pro Ser Lys Ile Thr Lys Phe Glu Asn Ala Phe Leu  
10 500 505 510  
Ser His Val Val Ser Gln His Gln Ala Leu Leu Gly Thr Ile Arg Ala  
515 520 525  
Asp Gly Lys Ile Ser Glu Gln Ser Asp Ala Lys Leu Lys Glu Ile Val  
530 535 540  
15 Thr Asn Phe Leu Ala Gly Phe Glu Ala  
545 550

&lt;210&gt; 91

20 &lt;211&gt; 742

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Bile-salt-activated lipase precursor

&lt;222&gt; (1) .. (742)

&lt;223&gt; Accession No. as of 29 August 2003: P19835

&lt;400&gt; 91

5 Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys Cys Trp Ala  
1 5 10 15  
Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe  
20 25 30  
Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp  
10 35 40 45  
Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn  
50 55 60  
Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe  
65 70 75 80  
15 Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly  
85 90 95  
Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys  
100 105 110  
Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala  
20 115 120 125  
Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu  
130 135 140  
Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr  
145 150 155 160

277/335

Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala  
165 170 175

Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala  
180 185 190

5 Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile  
195 200 205

Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr  
210 215 220

Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser  
10 225 230 235 240

Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp  
245 250 255

Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala  
260 265 270

15 Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu  
275 280 285

Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr  
290 295 300

Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro  
20 305 310 315 320

Ile Asn Leu Tyr Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr  
325 330 335

Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile  
340 345 350

278/335

Asn Lys Gly Asn Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val  
355 360 365

Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe  
370 375 380

5 Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys  
385 390 395 400

Lys Lys Thr Val Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro  
405 410 415

Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys  
10 420 425 430

Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro  
435 440 445

Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly  
450 455 460

15 Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val  
465 470 475 480

Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp  
485 490 495

Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr  
20 500 505 510

Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser  
515 520 525

Ser Met Lys Arg Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu  
530 535 540



279/335

Thr Tyr Leu Ala Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val  
545 550 555 560  
Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp  
565 570 575  
5 Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro  
580 585 590  
Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly  
595 600 605  
Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro  
10 610 615 620  
Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr  
625 630 635 640  
Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala  
645 650 655  
15 Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Pro Val Pro Pro  
660 665 670  
Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly  
675 680 685  
Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro  
20 690 695 700  
Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser  
705 710 715 720  
Glu Ala Ala Pro Val Pro Pro Thr Asp Asp Ser Lys Glu Ala Gln Met  
725 730 735

Pro Ala Val Ile Arg Phe

740

5 <210> 92

<211> 467

<212> PRT

<213> Homo sapiens

<220>

10 <221> Pancreatic lipase related protein precursor

<222> (1)..(467)

<223> Accession No. as of 29 August 2003: P54315

<400> 92

15 Met Leu Ile Phe Trp Thr Ile Thr Leu Phe Leu Leu Gly Ala Ala Lys

1 5 10 15

Gly Lys Glu Val Cys Tyr Glu Asp Leu Gly Cys Phe Ser Asp Thr Glu

20 25 30

Pro Trp Gly Gly Thr Ala Ile Arg Pro Leu Lys Ile Leu Pro Trp Ser

20 35 40 45

Pro Glu Lys Ile Gly Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro

50 55 60

Asn Asn Phe Gln Ile Leu Leu Leu Ser Asp Pro Ser Thr Ile Glu Ala

65 70 75 80

281/335

Ser Asn Phe Gln Met Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe  
85 90 95

Ile Asp Lys Gly Asp Glu Ser Trp Val Thr Asp Met Cys Lys Lys Leu  
100 105 110

5 Phe Glu Val Glu Glu Val Asn Cys Ile Cys Val Asp Trp Lys Lys Gly  
115 120 125

Ser Gln Ala Thr Tyr Thr Gln Ala Ala Asn Asn Val Arg Val Val Gly  
130 135 140

Ala Gln Val Ala Gln Met Leu Asp Ile Leu Leu Thr Glu Tyr Ser Tyr  
10 145 150 155 160

Pro Pro Ser Lys Val His Leu Ile Gly His Ser Leu Gly Ala His Val  
165 170 175

Ala Gly Glu Ala Gly Ser Lys Thr Pro Gly Leu Ser Arg Ile Thr Gly  
180 185 190

15 Leu Asp Pro Val Glu Ala Ser Phe Glu Ser Thr Pro Glu Glu Val Arg  
195 200 205

Leu Asp Pro Ser Asp Ala Asp Phe Val Asp Val Ile His Thr Asp Ala  
210 215 220

Ala Pro Leu Ile Pro Phe Leu Gly Phe Gly Thr Asn Gln Gln Met Gly  
20 225 230 235 240

His Leu Asp Phe Phe Pro Asn Gly Gly Glu Ser Met Pro Gly Cys Lys  
245 250 255

Lys Asn Ala Leu Ser Gln Ile Val Asp Leu Asp Gly Ile Trp Ala Gly  
260 265 270

282/335

Thr Arg Asp Phe Val Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr  
275 280 285

Leu Glu Ser Ile Leu Asn Pro Asp Gly Phe Ala Ala Tyr Pro Cys Thr  
290 295 300

5 Ser Tyr Lys Ser Phe Glu Ser Asp Lys Cys Phe Pro Cys Pro Asp Gln  
305 310 315 320

Gly Cys Pro Gln Met Gly His Tyr Ala Asp Lys Phe Ala Gly Arg Thr  
325 330 335

Ser Glu Glu Gln Gln Lys Phe Phe Leu Asn Thr Gly Glu Ala Ser Asn  
10 340 345 350

Phe Ala Arg Trp Arg Tyr Gly Val Ser Ile Thr Leu Ser Gly Arg Thr  
355 360 365

Ala Thr Gly Gln Ile Lys Val Ala Leu Phe Gly Asn Lys Gly Asn Thr  
370 375 380

15 His Gln Tyr Ser Ile Phe Arg Gly Ile Leu Lys Pro Gly Ser Thr His  
385 390 395 400

Ser Tyr Glu Phe Asp Ala Lys Leu Asp Val Gly Thr Ile Glu Lys Val  
405 410 415

Lys Phe Leu Trp Asn Asn Asn Val Ile Asn Pro Thr Leu Pro Lys Val  
20 420 425 430

Gly Ala Thr Lys Ile Thr Val Gln Lys Gly Glu Glu Lys Thr Val Tyr  
435 440 445

Asn Phe Cys Ser Glu Asp Thr Val Arg Glu Asp Thr Leu Leu Thr Leu  
450 455 460

Thr Pro Cys

465

5 &lt;210&gt; 93

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

10 &lt;221&gt; Pancreatic lipase related protein 2 precursor

&lt;222&gt; (1)..(469)

&lt;223&gt; Accession No. as of 29 August 2003: P54317

&lt;400&gt; 93

15 Met Leu Pro Pro Trp Thr Leu Gly Leu Leu Leu Leu Ala Thr Val Arg

1 5 10 15

Gly Lys Glu Val Cys Tyr Gly Gln Leu Gly Cys Phe Ser Asp Glu Lys

20 25 30

Pro Trp Ala Gly Thr Leu Gln Arg Pro Val Lys Leu Leu Pro Trp Ser

20 35 40 45

Pro Glu Asp Ile Asp Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro

50 55 60

Asn Asn Phe Gln Leu Ile Thr Gly Thr Glu Pro Asp Thr Ile Glu Ala

65 70 75 80

284/335

Ser Asn Phe Gln Leu Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe  
85 90 95

Leu Asp Lys Ala Glu Asp Ser Trp Pro Ser Asp Met Cys Lys Lys Met  
100 105 110

5 Phe Glu Val Glu Lys Val Asn Cys Ile Cys Val Asp Trp Arg His Gly  
115 120 125

Ser Arg Ala Met Tyr Thr Gln Ala Val Gln Asn Ile Arg Val Val Gly  
130 135 140

Ala Glu Thr Ala Phe Leu Ile Gln Ala Leu Ser Thr Gln Leu Gly Tyr  
10 145 150 155 160

Ser Leu Glu Asp Val His Val Ile Gly His Ser Leu Gly Ala His Thr  
165 170 175

Ala Ala Glu Ala Gly Arg Arg Leu Gly Gly Arg Val Gly Arg Ile Thr  
180 185 190

15 Gly Leu Asp Pro Ala Gly Pro Cys Phe Gln Asp Glu Pro Glu Glu Val  
195 200 205

Arg Leu Asp Pro Ser Asp Ala Val Phe Val Asp Val Ile His Thr Asp  
210 215 220

Ser Ser Pro Ile Val Pro Ser Leu Gly Phe Gly Met Ser Gln Lys Val  
20 225 230 235 240

Gly His Leu Asp Phe Phe Pro Asn Gly Gly Lys Glu Met Pro Gly Cys  
245 250 255

Lys Lys Asn Val Leu Ser Thr Ile Thr Asp Ile Asp Gly Ile Trp Glu  
260 265 270

285/335

Gly Ile Gly Gly Phe Val Ser Cys Asn His Leu Arg Ser Phe Glu Tyr  
275 280 285

Tyr Ser Ser Ser Val Leu Asn Pro Asp Gly Phe Leu Gly Tyr Pro Cys  
290 295 300

5 Ala Ser Tyr Asp Glu Phe Gln Glu Ser Lys Cys Phe Pro Cys Pro Ala  
305 310 315 320

Glu Gly Cys Pro Lys Met Gly His Tyr Ala Asp Gln Phe Lys Gly Lys  
325 330 335

Thr Ser Ala Val Glu Gln Thr Phe Phe Leu Asn Thr Gly Glu Ser Gly  
10 340 345 350

Asn Phe Thr Ser Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys  
355 360 365

Glu Lys Val Asn Gly Tyr Ile Arg Ile Ala Leu Tyr Gly Ser Asn Glu  
370 375 380

15 Asn Ser Lys Gln Tyr Glu Ile Phe Lys Gly Ser Leu Lys Pro Asp Ala  
385 390 395 400

Ser His Thr Cys Ala Ile Asp Val Asp Phe Asn Val Gly Lys Ile Gln  
405 410 415

Lys Val Lys Phe Leu Trp Asn Lys Arg Gly Ile Asn Leu Ser Glu Pro  
20 420 425 430

Lys Leu Gly Ala Ser Gln Ile Thr Val Gln Ser Gly Glu Asp Gly Thr  
435 440 445

Glu Tyr Asn Phe Cys Ser Ser Asp Thr Val Glu Glu Asn Val Leu Gln  
450 455 460

Ser Leu Tyr Pro Cys

465

5 <210> 94

<211> 465

<212> PRT

<213> Homo sapiens

<220>

10 <221> Triacylglycerol lipase, pancreatic precursor

<222> (1)..(465)

<223> Accession No. as of 29 August 2003: P16233

<400> 94

15 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly

1 5 10 15

Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe Ser Asp Asp Ser Pro

20 25 30

Trp Ser Gly Ile Thr Glu Arg Pro Leu His Ile Leu Pro Trp Ser Pro

20 35 40 45

Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn

50 55 60

Asn Phe Gln Glu Val Ala Ala Asp Ser Ser Ser Ile Ser Gly Ser Asn

65 70 75 80



287/335

Phe Lys Thr Asn Arg Lys Thr Arg Phe Ile Ile His Gly Phe Ile Asp  
 85 90 95  
 Lys Gly Glu Glu Asn Trp Leu Ala Asn Val Cys Lys Asn Leu Phe Lys  
 100 105 110  
 5 Val Glu Ser Val Asn Cys Ile Cys Val Asp Trp Lys Gly Gly Ser Arg  
 115 120 125  
 Thr Gly Tyr Thr Gln Ala Ser Gln Asn Ile Arg Ile Val Gly Ala Glu  
 130 135 140  
 Val Ala Tyr Phe Val Glu Phe Leu Gln Ser Ala Phe Gly Tyr Ser Pro  
 10 145 150 155 160  
 Ser Asn Val His Val Ile Gly His Ser Leu Gly Ala His Ala Ala Gly  
 165 170 175  
 Glu Ala Gly Arg Arg Thr Asn Gly Thr Ile Gly Arg Ile Thr Gly Leu  
 180 185 190  
 15 Asp Pro Ala Glu Pro Cys Phe Gln Gly Thr Pro Glu Leu Val Arg Leu  
 195 200 205  
 Asp Pro Ser Asp Ala Lys Phe Val Asp Val Ile His Thr Asp Gly Ala  
 210 215 220  
 Pro Ile Val Pro Asn Leu Gly Phe Gly Met Ser Gln Val Val Gly His  
 20 225 230 235 240  
 Leu Asp Phe Phe Pro Asn Gly Gly Val Glu Met Pro Gly Cys Lys Lys  
 245 250 255  
 Asn Ile Leu Ser Gln Ile Val Asp Ile Asp Gly Ile Trp Glu Gly Thr  
 260 265 270

288/335

Arg Asp Phe Ala Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr Thr  
275 280 285

Asp Ser Ile Val Asn Pro Asp Gly Phe Ala Gly Phe Pro Cys Ala Ser  
290 295 300

5 Tyr Asn Val Phe Thr Ala Asn Lys Cys Phe Pro Cys Pro Ser Gly Gly  
305 310 315 320

Cys Pro Gln Met Gly His Tyr Ala Asp Arg Tyr Pro Gly Lys Thr Asn  
325 330 335

Asp Val Gly Gln Lys Phe Tyr Leu Asp Thr Gly Asp Ala Ser Asn Phe  
10 340 345 350

Ala Arg Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys Lys Val  
355 360 365

Thr Gly His Ile Leu Val Ser Leu Phe Gly Asn Lys Gly Asn Ser Lys  
370 375 380

15 Gln Tyr Glu Ile Phe Lys Gly Thr Leu Lys Pro Asp Ser Thr His Ser  
385 390 395 400

Asn Glu Phe Asp Ser Asp Val Asp Val Gly Asp Leu Gln Met Val Lys  
405 410 415

Phe Ile Trp Tyr Asn Asn Val Ile Asn Pro Thr Leu Pro Arg Val Gly  
20 420 425 430

Ala Ser Lys Ile Ile Val Glu Thr Asn Val Gly Lys Gln Phe Asn Phe  
435 440 445

Cys Ser Pro Glu Thr Val Arg Glu Glu Val Leu Leu Thr Leu Thr Pro  
450 455 460

Cys

465

5 &lt;210&gt; 95

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

10 &lt;221&gt; Dihydropyrimidinase related protein-2

&lt;222&gt; (1)..(572)

&lt;223&gt; Accession No. as of 29 August 2003: Q16555

&lt;400&gt; 95

15 Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg

1 5 10 15

Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr

20 25 30

Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn

20 35 40 45

Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met

50 55 60

Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp

65 70 75 80

290/335

Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala  
85 90 95

Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro  
100 105 110

5 Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp  
115 120 125

Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp  
130 135 140

His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly  
10 145 150 155 160

Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu  
165 170 175

Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly  
180 185 190

15 Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu  
195 200 205

Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val  
210 215 220

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile  
20 225 230 235 240

Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met  
245 250 255

Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr  
260 265 270

291/335

Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser  
275 280 285

His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Phe Val Thr Ser  
290 295 300

5 Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu  
305 310 315 320

Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe  
325 330 335

Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro  
10 340 345 350

Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys  
355 360 365

Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr  
370 375 380

15 Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg  
385 390 395 400

Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser  
405 410 415

Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn  
20 420 425 430

Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser  
435 440 445

Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly  
450 455 460

292/335

Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys  
465 470 475 480  
Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg  
485 490 495  
5 Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr  
500 505 510  
Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala  
515 520 525  
Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala  
10 530 535 540  
Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala  
545 550 555 560  
Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly  
565 570

15

&lt;210&gt; 96

&lt;211&gt; 500

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; 4-aminobutyrate aminotransferase, mitochondrial precursor

&lt;222&gt; (1)..(500)

&lt;223&gt; Accession No. as of 29 August 2003: P80404

293/335

&lt;400&gt; 96

Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His  
1 5 10 15  
5 Thr Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala  
20 25 30  
Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr  
35 40 45  
Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile  
10 50 55 60  
Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser  
65 70 75 80  
Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu  
85 90 95  
15 Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser Asp Pro Ala Leu  
100 105 110  
Val Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg  
115 120 125  
Pro Ala Leu Glu Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg  
20 130 135 140  
Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr  
145 150 155 160  
Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe  
165 170 175

294/335

Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Lys Glu  
180 185 190  
Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Trp Cys Pro Asp Tyr  
195 200 205  
5 Ser Ile Leu Ser Phe Met Gly Ser Phe His Gly Arg Thr Met Gly Cys  
210 215 220  
Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser  
225 230 235 240  
Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu  
10 245 250 255  
Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Gly Cys Leu Glu Glu  
260 265 270  
Val Glu Asp Leu Ile Val Lys Tyr Arg Lys Lys Lys Lys Thr Val Ala  
275 280 285  
15 Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala  
290 295 300  
Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Cys  
305 310 315 320  
Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly  
20 325 330 335  
Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val  
340 345 350  
Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe Leu Lys Glu  
355 360 365



295/335

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly  
370 375 380  
Asp Pro Ser Lys Asn Leu Leu Leu Ala Glu Val Ile Asn Ile Ile Lys  
385 390 395 400  
5 Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu  
405 410 415  
Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg  
420 425 430  
Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser  
10 435 440 445  
Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu  
450 455 460  
Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe  
465 470 475 480  
15 Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu  
485 490 495  
Ala Asp Phe Lys  
500

20

&lt;210&gt; 97

&lt;211&gt; 423

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Glycine amidiontransferase, mitochondrial precursor

&lt;222&gt; (1)..(423)

&lt;223&gt; Accession No. as of 29 August 2003: P50440

5 &lt;400&gt; 97

Met Leu Arg Val Arg Cys Leu Arg Gly Gly Ser Arg Gly Ala Glu Ala  
1 5 10 15  
Val His Tyr Ile Gly Ser Arg Leu Gly Arg Thr Leu Thr Gly Trp Val  
10 20 25 30  
Gln Arg Thr Phe Gln Ser Thr Gln Ala Ala Thr Ala Ser Ser Arg Asn  
35 40 45  
Ser Cys Ala Ala Asp Asp Lys Ala Thr Glu Pro Leu Pro Lys Asp Cys  
50 55 60  
15 Pro Val Ser Ser Tyr Asn Glu Trp Asp Pro Leu Glu Glu Val Ile Val  
65 70 75 80  
Gly Arg Ala Glu Asn Ala Cys Val Pro Pro Phe Thr Ile Glu Val Lys  
85 90 95  
Ala Asn Thr Tyr Glu Lys Tyr Trp Pro Phe Tyr Gln Lys Gln Gly Gly  
20 100 105 110  
His Tyr Phe Pro Lys Asp His Leu Lys Lys Ala Val Ala Glu Ile Glu  
115 120 125  
Glu Met Cys Asn Ile Leu Lys Thr Glu Gly Val Thr Val Arg Arg Pro  
130 135 140

297/335

Asp Pro Ile Asp Trp Ser Leu Lys Tyr Lys Thr Pro Asp Phe Glu Ser  
145 150 155 160  
Thr Gly Leu Tyr Ser Ala Met Pro Arg Asp Ile Leu Ile Val Val Gly  
165 170 175  
5 Asn Glu Ile Ile Glu Ala Pro Met Ala Trp Arg Ser Arg Phe Phe Glu  
180 185 190  
Tyr Arg Ala Tyr Arg Ser Ile Ile Lys Asp Tyr Phe His Arg Gly Ala  
195 200 205  
Lys Trp Thr Thr Ala Pro Lys Pro Thr Met Ala Asp Glu Leu Tyr Asn  
10 210 215 220  
Gln Asp Tyr Pro Ile His Ser Val Glu Asp Arg His Lys Leu Ala Ala  
225 230 235 240  
Gln Gly Lys Phe Val Thr Thr Glu Phe Glu Pro Cys Phe Asp Ala Ala  
245 250 255  
15 Asp Phe Ile Arg Ala Gly Arg Asp Ile Phe Ala Gln Arg Ser Gln Val  
260 265 270  
Thr Asn Tyr Leu Gly Ile Glu Trp Met Arg Arg His Leu Ala Pro Asp  
275 280 285  
Tyr Arg Val His Ile Ile Ser Phe Lys Asp Pro Asn Pro Met His Ile  
20 290 295 300  
Asp Ala Thr Phe Asn Ile Ile Gly Pro Gly Ile Val Leu Ser Asn Pro  
305 310 315 320  
Asp Arg Pro Cys His Gln Ile Asp Leu Phe Lys Lys Ala Gly Trp Thr  
325 330 335

298/335

Ile Ile Thr Pro Pro Thr Pro Ile Ile Pro Asp Asp His Pro Leu Trp  
340 345 350  
Met Ser Ser Lys Trp Leu Ser Met Asn Val Leu Met Leu Asp Glu Lys  
355 360 365  
5 Arg Val Met Val Asp Ala Asn Glu Val Pro Ile Gln Lys Met Phe Glu  
370 375 380  
Lys Leu Gly Ile Thr Thr Ile Lys Val Asn Ile Arg Asn Ala Asn Ser  
385 390 395 400  
Leu Gly Gly Gly Phe His Cys Trp Thr Cys Asp Val Arg Arg Arg Gly  
10 405 410 415  
Thr Leu Gln Ser Tyr Leu Asp  
420

15 &lt;210&gt; 98

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

20 &lt;221&gt; GRP 78

&lt;222&gt; (1)..(654)

&lt;223&gt; Accession No. as of 29 August 2003: P11021

&lt;220&gt;

&lt;221&gt; misc\_feature

- <222> (302) .. (302)
- <223> Xaa can be any naturally occurring amino acid
- <220>
- <221> misc\_feature
- 5 <222> (329) .. (329)
- <223> Xaa can be any naturally occurring amino acid
- <220>
- <221> misc\_feature
- <222> (344) .. (344)
- 10 <223> Xaa can be any naturally occurring amino acid
- <220>
- <221> misc\_feature
- <222> (461) .. (461)
- <223> Xaa can be any naturally occurring amino acid
- 15 <400> 98

Met Lys Leu Ser Leu Val Ala Ala Met Leu Leu Leu Leu Leu Ser Ala  
1 5 10 15  
Ala Arg Ala Lys Glu Glu Asp Met Gly Thr Val Val Ala Ile His Leu  
20 20 25 30  
Gly Thr Thr Tyr Pro Cys Val Gly Val Phe Lys Asn Gly Arg Met Glu  
35 40 45  
Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Met Pro Ser Tyr Val Ala  
50 55 60

300/335

Phe Thr Pro Glu Gly Glu Cys Leu Ile Gly Asp Ala Ala Lys Asn Gln  
65 70 75 80  
Leu Thr Ser Asn Pro Lys Asn Thr Val Phe Asp Ala Lys Arg Leu Ile  
85 90 95  
5 Gly Arg Arg Trp His Asp Pro Ser Val Gln Gln Asp Ile Glu Phe Leu  
100 105 110  
Pro Phe Lys Val Val Glu Lys Asn Thr Lys Ser Tyr Ile Gln Ile Asp  
115 120 125  
Val Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Lys Glu Ile Ser Ala  
10 130 135 140  
Met Val Leu Thr Lys Met Lys Glu Asn Ala Glu Ala Tyr Leu Gly Lys  
145 150 155 160  
Val Thr His Ala Val Val Thr Ala Pro Ala Tyr Phe Asn Asp Ala Gln  
165 170 175  
15 Cys Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Asp Leu Asn Val Met  
180 185 190  
Arg Ile Ile Asn Lys Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp  
195 200 205  
Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly Gly Gly  
20 210 215 220  
Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe Lys Val  
225 230 235 240  
Val Ala Thr Asn Gly Asp Thr Tyr Leu Gly Gly Glu Asp Phe Asp Gln  
245 250 255

301/335

Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr Gly Lys  
260 265 270

Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Trp Arg Lys Val  
275 280 285

5 Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Xaa Val Ile  
290 295 300

Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu Thr  
305 310 315 320

Gln Ala Lys Phe Glu Glu Leu Asn Xaa Asp Leu Phe Gln Ser Thr Met  
10 325 330 335

Lys Pro Ser Gln Arg Ser Val Xaa Lys Val Leu Glu Asp Ser Asp Leu  
340 345 350

Lys Lys Ser Asp Ile Asp Glu Thr Val Leu Val Gly Gly Phe Thr Gln  
355 360 365

15 Ile Pro Lys Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu  
370 375 380

Leu Ser Arg Gly Ile Ser Pro Tyr Glu Ala Val Ala Tyr Gly Ala Ala  
385 390 395 400

Val Gln Ala Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val  
20 405 410 415

Leu Leu Asp Ile Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly  
420 425 430

Val Met Thr Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys  
435 440 445

Ser Gln Ile Phe Ser Thr Ala Phe Asp Asn Gln Pro Xaa Thr Ile Lys  
450 455 460

Val Tyr Glu Gly Lys Gln Pro Leu Thr Lys Asp Asn His Leu Leu Gly  
465 470 475 480

5 Thr Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Cys Gly Val Pro Gln  
485 490 495

Ile Glu Val Thr Phe Glu Met Asp Val Ser Asp Ile Leu Gln Val Thr  
500 505 510

Ala Lys Asp Lys Gly Thr Arg Tyr Lys Asn Lys Ile Thr Ile Thr Asn  
10 515 520 525

Asp Gln Asn His Leu Thr Pro Glu Asp Ile Glu Arg Met Val Asn Asp  
530 535 540

Ala Glu Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Cys Thr Asp  
545 550 555 560

15 Thr Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile  
565 570 575

Gly Asp Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu  
580 585 590

Thr Met Glu Lys Thr Val Glu Glu Lys Thr Glu Trp Leu Glu Ser His  
20 595 600 605

Gln Asp Ala Asp Thr Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu  
610 615 620

Glu Ile Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro  
625 630 635 640



303/335

Pro Pro Thr Gly Glu Glu Asp Thr Ala Glu Lys Asp Glu Leu

645

650

5 &lt;210&gt; 99

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

10 &lt;221&gt; Eukaryotic translation initiation factor 3 subunit 2

&lt;222&gt; (1)..(325)

&lt;223&gt; Accession No. as of 29 August 2003: Q13347

&lt;400&gt; 99

15 Met Lys Pro Ile Leu Leu Gln Gly His Glu Arg Ser Ile Thr Gln Ile

1

5

10

15

Lys Tyr Asn Arg Glu Gly Asp Leu Leu Phe Thr Val Ala Lys Asp Pro

20

25

30

Ile Val Asn Val Trp Tyr Ser Val Asn Gly Glu Arg Leu Gly Thr Tyr

20

35

40

45

Met Gly His Thr Gly Ala Val Trp Cys Val Asp Ala Asp Trp Asp Thr

50

55

60

Lys His Val Leu Thr Gly Ser Ala Asp Asn Ser Cys Arg Leu Trp Asp

65

70

75

80

304/335

Cys Glu Thr Gly Lys Gln Leu Ala Leu Leu Lys Thr Asn Ser Ala Val  
85 90 95

Arg Thr Cys Gly Phe Asp Phe Gly Gly Asn Ile Ile Met Phe Ser Thr  
100 105 110

5 Asp Lys Gln Met Gly Tyr Gln Cys Phe Val Ser Phe Phe Asp Leu Arg  
115 120 125

Asp Pro Ser Gln Ile Asp Asn Asn Glu Pro Tyr Met Lys Ile Pro Cys  
130 135 140

Asn Asp Ser Lys Ile Thr Ser Ala Val Trp Gly Pro Leu Gly Glu Cys  
10 145 150 155 160

Ile Ile Ala Gly His Glu Ser Gly Glu Leu Asn Gln Tyr Ser Ala Lys  
165 170 175

Ser Gly Glu Val Leu Val Asn Val Lys Glu His Ser Arg Gln Ile Asn  
180 185 190

15 Asp Ile Gln Leu Ser Arg Asp Met Thr Met Phe Val Thr Ala Ser Lys  
195 200 205

Asp Asn Thr Ala Lys Leu Phe Asp Ser Thr Thr Leu Glu His Gln Lys  
210 215 220

Thr Phe Arg Thr Glu Arg Pro Val Asn Ser Ala Ala Leu Ser Pro Asn  
20 225 230 235 240

Tyr Asp His Val Val Leu Gly Gly Gly Gln Glu Ala Met Asp Val Thr  
245 250 255

Thr Thr Ser Thr Arg Ile Gly Lys Phe Glu Ala Arg Phe Phe His Leu  
260 265 270

305/335

Ala Phe Glu Glu Glu Phe Gly Arg Val Lys Gly His Phe Gly Pro Ile

275

280

285

Asn Ser Val Ala Phe His Pro Asp Gly Lys Ser Tyr Ser Ser Gly Gly

290

295

300

5 Glu Asp Gly Tyr Val Arg Ile His Tyr Phe Asp Pro Gln Tyr Phe Glu

305

310

315

320

Phe Glu Phe Glu Ala

325

10

&lt;210&gt; 100

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15 &lt;220&gt;

&lt;221&gt; Dihydropyrimidinase related protein-2

&lt;222&gt; (1)..(572)

&lt;223&gt; Accession No. as of 29 August 2003: Q16555

&lt;400&gt; 100

20

Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg

1

5

10

15

Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr

20

25

30

306/335

Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn  
35 40 45

Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met  
50 55 60

5 Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp  
65 70 75 80

Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala  
85 90 95

Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro  
10 100 105 110

Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp  
115 120 125

Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp  
130 135 140

15 His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly  
145 150 155 160

Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu  
165 170 175

Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly  
20 180 185 190

Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu  
195 200 205

Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val  
210 215 220

307/335

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile  
 225 230 235 240  
 Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met  
 245 250 255  
 5 Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr  
 260 265 270  
 Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser  
 275 280 285  
 His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Ala Phe Val Thr Ser  
 10 290 295 300  
 Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu  
 305 310 315 320  
 Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe  
 325 330 335  
 15 Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro  
 340 345 350  
 Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys  
 355 360 365  
 Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr  
 20 370 375 380  
 Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg  
 385 390 395 400  
 Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser  
 405 410 415

308/335

Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn  
420 425 430  
Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser  
435 440 445  
5 Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly  
450 455 460  
Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys  
465 470 475 480  
Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg  
10 485 490 495  
Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr  
500 505 510  
Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala  
515 520 525  
15 Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala  
530 535 540  
Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala  
545 550 555 560  
Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly  
20 565 570

&lt;210&gt; 101

&lt;211&gt; 561

<212> PRT  
<213> Homo sapiens  
<220>  
<221> Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM)  
5 <222> (1)..(561)  
<223> Accession No. as of 29 August 2003: P36871  
<400> 101

Val Lys Ile Val Thr Val Lys Thr Gln Ala Tyr Gln Asp Gln Lys Pro  
10 1 5 10 15  
Gly Thr Ser Gly Leu Arg Lys Arg Val Lys Val Phe Gln Ser Ser Ala  
20 25 30  
Asn Tyr Ala Glu Asn Phe Ile Gln Ser Ile Ile Ser Thr Val Glu Pro  
35 40 45  
15 Ala Gln Arg Gln Glu Ala Thr Leu Val Val Gly Gly Asp Gly Arg Phe  
50 55 60  
Tyr Met Lys Glu Ala Ile Gln Leu Ile Ala Arg Ile Ala Ala Ala Asn  
65 70 75 80  
Gly Ile Gly Arg Leu Val Ile Gly Gln Asn Gly Ile Leu Ser Thr Pro  
20 85 90 95  
Ala Val Ser Cys Ile Ile Arg Lys Ile Lys Ala Ile Gly Gly Ile Ile  
100 105 110  
Leu Thr Ala Ser His Asn Pro Gly Gly Pro Asn Gly Asp Phe Gly Ile  
115 120 125

310/335

Lys Phe Asn Ile Ser Asn Gly Gly Pro Ala Pro Glu Ala Ile Thr Asp  
130 135 140

Lys Ile Phe Gln Ile Ser Lys Thr Ile Glu Glu Tyr Ala Val Cys Pro  
145 150 155 160

5 Asp Leu Lys Val Asp Leu Gly Val Leu Gly Lys Gln Gln Phe Asp Leu  
165 170 175

Glu Asn Lys Phe Lys Pro Phe Thr Val Glu Ile Val Asp Ser Val Glu  
180 185 190

Ala Tyr Ala Thr Met Leu Arg Ser Ile Phe Asp Phe Ser Ala Leu Lys  
10 195 200 205

Glu Leu Leu Ser Gly Pro Asn Arg Leu Lys Ile Arg Ile Asp Ala Met  
210 215 220

His Gly Val Val Gly Pro Tyr Val Lys Lys Ile Leu Cys Glu Glu Leu  
225 230 235 240

15 Gly Ala Pro Ala Asn Ser Ala Val Asn Cys Val Pro Leu Glu Asp Phe  
245 250 255

Gly Gly His His Pro Asp Pro Asn Leu Thr Tyr Ala Ala Asp Leu Val  
260 265 270

Glu Thr Met Lys Ser Gly Glu His Asp Phe Gly Ala Ala Phe Asp Gly  
20 275 280 285

Asp Gly Asp Arg Asn Met Ile Leu Gly Lys His Gly Phe Phe Val Asn  
290 295 300

Pro Ser Asp Ser Val Ala Val Ile Ala Ala Asn Ile Phe Ser Ile Pro  
305 310 315 320



311/335

Tyr Phe Gln Gln Thr Gly Val Arg Gly Phe Ala Arg Ser Met Pro Thr  
325 330 335

Ser Gly Ala Leu Asp Arg Val Ala Ser Ala Thr Lys Ile Ala Leu Tyr  
340 345 350

5 Glu Thr Pro Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Ser  
355 360 365

Lys Leu Ser Leu Cys Gly Glu Glu Ser Phe Gly Thr Gly Ser Asp His  
370 375 380

Ile Arg Glu Lys Asp Gly Leu Trp Ala Val Leu Ala Trp Leu Ser Ile  
10 385 390 395 400

Leu Ala Thr Arg Lys Gln Ser Val Glu Asp Ile Leu Lys Asp His Trp  
405 410 415

Gln Lys Tyr Gly Arg Asn Phe Phe Thr Arg Tyr Asp Tyr Glu Glu Val  
420 425 430

15 Glu Ala Glu Gly Ala Asn Lys Met Met Lys Asp Leu Glu Ala Leu Met  
435 440 445

Phe Asp Arg Ser Phe Val Gly Lys Gln Phe Ser Ala Asn Asp Lys Val  
450 455 460

Tyr Thr Val Glu Lys Ala Asp Asn Phe Glu Tyr Ser Asp Pro Val Asp  
20 465 470 475 480

Gly Ser Ile Ser Arg Asn Gln Gly Leu Arg Leu Ile Phe Thr Asp Gly  
485 490 495

Ser Arg Ile Val Phe Arg Leu Ser Gly Thr Gly Ser Ala Gly Ala Thr  
500 505 510

312/335

Ile Arg Leu Tyr Ile Asp Ser Tyr Glu Lys Asp Val Ala Lys Ile Asn

515

520

525

Gln Asp Pro Gln Val Met Leu Ala Pro Leu Ile Ser Ile Ala Leu Lys

530

535

540

5 Val Ser Gln Leu Gln Glu Arg Thr Gly Arg Thr Ala Pro Thr Val Ile

545

550

555

560

Thr

10

&lt;210&gt; 102

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15 &lt;220&gt;

&lt;221&gt; Proteasome subunit alpha type 1

&lt;222&gt; (1)..(263)

&lt;223&gt; Accession No. as of 29 August 2003: P25786

&lt;400&gt; 102

20

Met Phe Arg Asn Gln Tyr Asp Asn Asp Val Thr Val Trp Ser Pro Gln

1

5

10

15

Gly Arg Ile His Gln Ile Glu Tyr Ala Met Glu Ala Val Lys Gln Gly

20

25

30

313/335

Ser Ala Thr Val Gly Leu Lys Ser Lys Thr His Ala Val Leu Val Ala  
35 40 45  
Leu Lys Arg Ala Gln Ser Glu Leu Ala Ala His Gln Lys Lys Ile Leu  
50 55 60  
5 His Val Asp Asn His Ile Gly Ile Ser Ile Ala Gly Leu Thr Ala Asp  
65 70 75 80  
Ala Arg Leu Leu Cys Asn Phe Met Arg Gln Glu Cys Leu Asp Ser Arg  
85 90 95  
Phe Val Phe Asp Arg Pro Leu Pro Val Ser Arg Leu Val Ser Leu Ile  
10 100 105 110  
Gly Ser Lys Thr Gln Ile Pro Thr Gln Arg Tyr Gly Arg Arg Pro Tyr  
115 120 125  
Gly Val Gly Leu Leu Ile Ala Gly Tyr Asp Asp Met Gly Pro His Ile  
130 135 140  
15 Phe Gln Thr Cys Pro Ser Ala Asn Tyr Phe Asp Cys Arg Ala Met Ser  
145 150 155 160  
Ile Gly Ala Arg Ser Gln Ser Ala Arg Thr Tyr Leu Glu Arg His Met  
165 170 175  
Ser Glu Phe Met Glu Cys Asn Leu Asn Glu Leu Val Lys His Gly Leu  
20 180 185 190  
Arg Ala Leu Arg Glu Thr Leu Pro Ala Glu Gln Asp Leu Thr Thr Lys  
195 200 205  
Asn Val Ser Ile Gly Ile Val Gly Lys Asp Leu Glu Phe Thr Ile Tyr  
210 215 220

314/335

Asp Asp Asp Asp Val Ser Pro Phe Leu Glu Gly Leu Glu Glu Arg Pro

225                      230                      235                      240

Gln Arg Lys Ala Gln Pro Ala Gln Pro Ala Asp Glu Pro Ala Glu Lys

245                      250                      255

5    Ala Asp Glu Pro Met Glu His

260

<210> 103

10 <211> 205

<212> PRT

<213> Homo sapiens

<220>

<221> Heat shock 27 kDa protein

15 <222> (1)..(205)

<223> Accession No. as of 29 August 2003: P04792

<400> 103

Met Thr Glu Arg Arg Val Pro Phe Ser Leu Leu Arg Gly Pro Ser Trp

20    1                      5                      10                      15

Asp Pro Phe Arg Asp Trp Tyr Pro His Ser Arg Leu Phe Asp Gln Ala

20                      25                      30

Phe Gly Leu Pro Arg Leu Pro Glu Glu Trp Ser Gln Trp Leu Gly Gly

35

40

45

315/335

Ser Ser Trp Pro Gly Tyr Val Arg Pro Leu Pro Pro Ala Ala Ile Glu  
50 55 60  
Ser Pro Ala Val Ala Ala Pro Ala Tyr Ser Arg Ala Leu Ser Arg Gln  
65 70 75 80  
5 Leu Ser Ser Gly Val Ser Glu Ile Arg His Thr Ala Asp Arg Trp Arg  
85 90 95  
Val Ser Leu Asp Val Asn His Phe Ala Pro Asp Glu Leu Thr Val Lys  
100 105 110  
Thr Lys Asp Gly Val Val Glu Ile Thr Gly Lys His Glu Glu Arg Gln  
10 115 120 125  
Asp Glu His Gly Tyr Ile Ser Arg Cys Phe Thr Arg Lys Tyr Thr Leu  
130 135 140  
Pro Pro Gly Val Asp Pro Thr Gln Val Ser Ser Ser Leu Ser Pro Glu  
145 150 155 160  
15 Gly Thr Leu Thr Val Glu Ala Pro Met Pro Lys Leu Ala Thr Gln Ser  
165 170 175  
Asn Glu Ile Thr Ile Pro Val Thr Phe Glu Ser Arg Ala Gln Leu Gly  
180 185 190  
Gly Pro Glu Ala Ala Lys Ser Asp Glu Thr Ala Ala Lys  
20 195 200 205

&lt;210&gt; 104

&lt;211&gt; 868

316/335

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Programmed cell death 6 interacting protein (Hp95)

5 &lt;222&gt; (1)..(868)

&lt;223&gt; Accession No. as of 29 August 2003: Q8WUM4

&lt;400&gt; 104

Met Ala Thr Phe Ile Ser Val Gln Leu Lys Lys Thr Ser Glu Val Asp  
10 1 5 10 15  
Leu Ala Lys Pro Leu Val Lys Phe Ile Gln Gln Thr Tyr Pro Ser Gly  
20 25 30  
Gly Glu Glu Gln Ala Gln Tyr Cys Arg Ala Ala Glu Glu Leu Ser Lys  
35 40 45  
15 Leu Arg Arg Ala Ala Val Gly Arg Pro Leu Asp Lys His Glu Gly Ala  
50 55 60  
Leu Glu Thr Leu Leu Arg Tyr Tyr Asp Gln Ile Cys Ser Ile Glu Pro  
65 70 75 80  
Lys Phe Pro Phe Ser Glu Asn Gln Ile Cys Leu Thr Phe Thr Trp Lys  
20 85 90 95  
Asp Ala Phe Asp Lys Gly Ser Leu Phe Gly Gly Ser Val Lys Leu Ala  
100 105 110  
Leu Ala Ser Leu Gly Tyr Glu Lys Ser Cys Val Leu Phe Asn Cys Ala  
115 120 125

317/335

Ala Leu Ala Ser Gln Ile Ala Ala Glu Gln Asn Leu Asp Asn Asp Glu  
130 135 140  
Gly Leu Lys Ile Ala Ala Lys His Tyr Gln Phe Ala Ser Gly Ala Phe  
145 150 155 160  
5 Leu His Ile Lys Glu Thr Val Leu Ser Ala Leu Ser Arg Glu Pro Thr  
165 170 175  
Val Asp Ile Ser Pro Asp Thr Val Gly Thr Leu Ser Leu Ile Met Leu  
180 185 190  
Ala Gln Ala Gln Glu Val Phe Phe Leu Lys Ala Thr Arg Asp Lys Met  
10 195 200 205  
Lys Asp Ala Ile Ile Ala Lys Leu Ala Asn Gln Ala Ala Asp Tyr Phe  
210 215 220  
Gly Asp Ala Phe Lys Gln Cys Gln Tyr Lys Asp Thr Leu Pro Lys Glu  
225 230 235 240  
15 Val Phe Pro Val Leu Ala Ala Lys His Cys Ile Met Gln Ala Asn Ala  
245 250 255  
Glu Tyr His Gln Ser Ile Leu Ala Lys Gln Gln Lys Lys Phe Gly Glu  
260 265 270  
Glu Ile Ala Arg Leu Gln His Ala Ala Glu Leu Ile Lys Thr Val Ala  
20 275 280 285  
Ser Arg Tyr Asp Glu Tyr Val Asn Val Lys Asp Phe Ser Asp Lys Ile  
290 295 300  
Asn Arg Ala Leu Ala Ala Ala Lys Lys Asp Asn Asp Phe Ile Tyr His  
305 310 315 320

318/335

Asp Arg Val Pro Asp Leu Lys Asp Leu Asp Pro Ile Gly Lys Ala Thr  
325 330 335

Leu Val Lys Ser Thr Pro Val Asn Val Pro Ile Ser Gln Lys Phe Thr  
340 345 350

5 Asp Leu Phe Glu Lys Met Val Pro Val Ser Val Gln Gln Ser Leu Ala  
355 360 365

Ala Tyr Asn Gln Arg Lys Ala Asp Leu Val Asn Arg Ser Ile Ala Gln  
370 375 380

Met Arg Glu Ala Thr Thr Leu Ala Asn Gly Val Leu Ala Ser Leu Asn  
10 385 390 395 400

Leu Pro Ala Ala Ile Glu Asp Val Ser Gly Asp Thr Val Pro Gln Ser  
405 410 415

Ile Leu Thr Lys Ser Arg Ser Val Ile Glu Gln Gly Gly Ile Gln Thr  
420 425 430

15 Val Asp Gln Leu Ile Lys Glu Leu Pro Glu Leu Leu Gln Arg Asn Arg  
435 440 445

Glu Ile Leu Asp Glu Ser Leu Arg Leu Leu Asp Glu Glu Glu Ala Thr  
450 455 460

Asp Asn Asp Leu Arg Ala Lys Phe Lys Glu Arg Trp Gln Arg Thr Pro  
20 465 470 475 480

Ser Asn Glu Leu Tyr Lys Pro Leu Arg Ala Glu Gly Thr Asn Phe Arg  
485 490 495

Thr Val Leu Asp Lys Ala Val Gln Ala Asp Gly Gln Val Lys Glu Cys  
500 505 510



319/335

Tyr Gln Ser His Arg Asp Thr Ile Val Leu Leu Cys Lys Pro Glu Pro  
515 520 525  
Glu Leu Asn Ala Ala Ile Pro Ser Ala Asn Pro Ala Lys Thr Met Gln  
530 535 540  
5 Gly Ser Glu Val Val Asn Val Leu Lys Ser Leu Leu Ser Asn Leu Asp  
545 550 555 560  
Glu Val Lys Lys Glu Arg Glu Gly Leu Glu Asn Asp Leu Lys Ser Val  
565 570 575  
Asn Phe Asp Met Thr Ser Lys Phe Leu Thr Ala Leu Ala Gln Asp Gly  
10 580 585 590  
Val Ile Asn Glu Glu Ala Leu Ser Val Thr Glu Leu Asp Arg Val Tyr  
595 600 605  
Gly Gly Leu Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly  
610 615 620  
15 Leu Leu Lys Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys  
625 630 635 640  
Gln Ser Asn Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu  
645 650 655  
Ala Thr Ala Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu  
20 660 665 670  
Gly Thr Lys Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln  
675 680 685  
Asn Lys Cys Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu  
690 695 700

320/335

Leu Leu Lys Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro  
705 710 715 720  
Ser Ile Pro Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala  
725 730 735  
5 Pro Thr Pro Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro  
740 745 750  
Gln Pro Pro Ala Arg Pro Pro Pro Pro Val Leu Pro Ala Asn Arg Ala  
755 760 765  
Pro Ser Ala Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro  
10 770 775 780  
Ala Pro Ser Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly  
785 790 795 800  
Pro Pro Tyr Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro  
805 810 815  
15 Met Pro Met Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro  
820 825 830  
Tyr Pro Pro Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly  
835 840 845  
Pro Gln Gln Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr  
20 850 855 860  
Tyr Pro Gln Gln  
865

<210> 105

<211> 280

<212> PRT

<213> Homo sapiens

5 <220>

<221> Similar to four and a half LIM domains 3

<222> (1)..(280)

<223> Accession No. as of 29 August 2003: Q9BVA2

<400> 105

10

Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly

1 5 10 15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr

20 25 30

15 Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly

35 40 45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly

50 55 60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe

20 65 70 75 80

Thr Cys Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala

85 90 95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser

100 105 110

322/335

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu  
115 120 125

Cys Ser Gly Cys Glu Gln Pro Leu Gly Ser Arg Ser Phe Val Pro Asp  
130 135 140

5 Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Lys Phe Ala Pro  
145 150 155 160

Arg Cys Ala Arg Cys Ser Lys Thr Leu Thr Gln Gly Gly Val Thr Tyr  
165 170 175

Arg Asp Gln Pro Trp His Arg Glu Cys Leu Val Cys Thr Gly Cys Gln  
10 180 185 190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr  
195 200 205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys  
210 215 220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu  
225 230 235 240

Asp Arg His Trp His His Asn Cys Phe Ser Cys Ala Arg Cys Ser Thr  
245 250 255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys  
20 260 265 270

Gln Gly Cys Ser Gln Ala Gly Pro  
275 280

323/335

&lt;210&gt; 106

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5 &lt;220&gt;

&lt;221&gt; Skeletal muscle LIM-protein 2 (SLIM 2)

&lt;222&gt; (1)..(280)

&lt;223&gt; Accession No. as of 29 August 2003: Q13643

&lt;400&gt; 106

10

Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly

1 5 10 15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr

20 25 30

15 Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly

35 40 45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly

50 55 60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe

20 65 70 75 80

Thr Arg Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala

85 90 95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser

100 105 110

324/335

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu  
115 120 125

Cys Ile Gly Cys Glu Gln Pro Leu Gly Ser Arg Pro Phe Val Pro Asp  
130 135 140

5 Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Asn Phe Ala Pro  
145 150 155 160

Arg Cys Ala Arg Cys Thr Lys Thr Leu Thr Gln Gly Gly Leu Thr Tyr  
165 170 175

Arg Asp Leu Pro Trp His Pro Lys Cys Leu Val Cys Thr Gly Cys Gln  
10 180 185 190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr  
195 200 205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys  
210 215 220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu  
225 230 235 240

Asp Arg His Trp His His Asn Cys Phe Thr Cys Asp Arg Cys Ser Asn  
245 250 255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys  
20 260 265 270

Gln Gly Cys Ser Gln Ala Gly Pro  
275 280

<210> 107

<211> 133

<212> PRT

<213> Homo sapiens

5 <220>

<221> Cytochrome b5

<222> (1)..(133)

<223> Accession No. as of 29 August 2003: P00167

<400> 107

10

Ala Glu Gln Ser Asp Glu Ala Val Lys Tyr Tyr Thr Leu Glu Glu Ile

1 5 10 15

Gln Lys His Asn His Ser Lys Ser Thr Trp Leu Ile Leu His His Lys

20 25 30

15 Val Tyr Asp Leu Thr Lys Phe Leu Glu Glu His Pro Gly Gly Glu Glu

35 40 45

Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu Asp

50 55 60

Val Gly His Ser Thr Asp Ala Arg Glu Met Ser Lys Thr Phe Ile Ile

20 65 70 75 80

Gly Glu Leu His Pro Asp Asp Arg Pro Lys Leu Asn Lys Pro Pro Glu

85 90 95

Thr Leu Ile Thr Thr Ile Asp Ser Ser Ser Ser Trp Trp Thr Asn Trp

100 105 110

326/335

Val Ile Pro Ala Ile Ser Ala Val Ala Val Ala Leu Met Tyr Arg Leu

115

120

125

Tyr Met Ala Glu Asp

130

5

&lt;210&gt; 108

&lt;211&gt; 175

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Pancreatitis-associated protein 1 precursor

&lt;222&gt; (1)..(175)

&lt;223&gt; Accession No. as of 29 August 2003: Q06141

15 &lt;400&gt; 108

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser

1

5

10

15

Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu

20

20

25

30

Leu Pro Ser Ala Arg Ile Arg Cys Pro Lys Gly Ser Lys Ala Tyr Gly

35

40

45

Ser His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala

50

55

60



327/335

Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Val Ser Val Leu  
65 70 75 80  
Ser Gly Ala Glu Gly Ser Phe Val Ser Ser Leu Val Lys Ser Ile Gly  
85 90 95  
5 Asn Ser Tyr Ser Tyr Val Trp Ile Gly Leu His Asp Pro Thr Gln Gly  
100 105 110  
Thr Glu Pro Asn Gly Glu Gly Trp Glu Trp Ser Ser Ser Asp Val Met  
115 120 125  
Asn Tyr Phe Ala Trp Glu Arg Asn Pro Ser Thr Ile Ser Ser Pro Gly  
10 130 135 140  
His Cys Ala Ser Leu Ser Arg Ser Thr Ala Phe Leu Arg Trp Lys Asp  
145 150 155 160  
Tyr Asn Cys Asn Val Arg Leu Pro Tyr Val Cys Lys Phe Thr Asp  
165 170 175

15

&lt;210&gt; 109

&lt;211&gt; 1028

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Collagen alpha 1(VI) chain precursor

&lt;222&gt; (1)..(1028)

&lt;223&gt; Accession No. as of 29 August 2003: P12109

328/335

&lt;400&gt; 109

Met Arg Ala Ala Arg Ala Leu Leu Pro Leu Leu Leu Gln Ala Cys Trp  
1 5 10 15  
5 Thr Ala Ala Gln Asp Glu Pro Glu Thr Pro Arg Ala Val Ala Phe Gln  
20 25 30  
Asp Cys Pro Val Asp Leu Phe Phe Val Leu Asp Thr Ser Glu Ser Val  
35 40 45  
Ala Leu Arg Leu Lys Pro Tyr Gly Ala Leu Val Asp Lys Val Lys Ser  
10 50 55 60  
Phe Thr Lys Arg Phe Ile Asp Asn Leu Arg Asp Arg Tyr Tyr Arg Cys  
65 70 75 80  
Asp Arg Asn Leu Val Trp Asn Ala Gly Ala Leu His Tyr Ser Asp Glu  
85 90 95  
15 Val Glu Ile Ile Gln Gly Leu Thr Arg Met Pro Gly Gly Arg Asp Ala  
100 105 110  
Leu Lys Ser Ser Val Asp Ala Val Lys Tyr Phe Gly Lys Gly Thr Tyr  
115 120 125  
Thr Asp Cys Ala Ile Lys Lys Gly Leu Glu Gln Leu Leu Val Gly Gly  
20 130 135 140  
Ser His Leu Lys Glu Asn Lys Tyr Leu Ile Val Val Thr Asp Gly His  
145 150 155 160  
Pro Leu Glu Gly Tyr Lys Glu Pro Cys Gly Gly Leu Glu Asp Ala Val  
165 170 175

329/335

Asn Glu Ala Lys His Leu Gly Val Lys Val Phe Ser Val Ala Ile Thr  
180 185 190

Pro Asp His Leu Glu Pro Arg Leu Ser Ile Ile Ala Thr Asp His Thr  
195 200 205

5 Tyr Arg Arg Asn Phe Thr Ala Ala Asp Trp Gly Gln Ser Arg Asp Ala  
210 215 220

Glu Glu Ala Ile Ser Gln Thr Ile Asp Thr Ile Val Asp Met Ile Lys  
225 230 235 240

Asn Asn Val Glu Gln Val Cys Cys Ser Phe Glu Cys Gln Pro Ala Arg  
10 245 250 255

Gly Pro Pro Gly Leu Arg Gly Asp Pro Gly Phe Glu Gly Glu Arg Gly  
260 265 270

Lys Pro Gly Leu Pro Gly Glu Lys Gly Glu Ala Gly Asp Pro Gly Arg  
275 280 285

15 Pro Gly Asp Leu Gly Pro Val Gly Tyr Gln Gly Met Lys Gly Glu Lys  
290 295 300

Gly Ser Arg Gly Glu Lys Gly Ser Arg Gly Pro Lys Gly Tyr Lys Gly  
305 310 315 320

Glu Lys Gly Lys Arg Gly Ile Asp Gly Val Asp Gly Val Lys Gly Glu  
20 325 330 335

Met Gly Tyr Pro Gly Leu Pro Gly Cys Lys Gly Ser Pro Gly Phe Asp  
340 345 350

Gly Ile Gln Gly Pro Pro Gly Pro Lys Gly Asp Pro Gly Ala Phe Gly  
355 360 365

330/335

Leu Lys Gly Glu Lys Gly Glu Pro Gly Ala Asp Gly Glu Ala Gly Arg  
370 375 380

Pro Gly Ala Arg Gly Pro Ser Gly Asp Glu Gly Pro Ala Gly Glu Pro  
385 390 395 400

5 Gly Pro Pro Gly Glu Lys Gly Glu Ala Gly Asp Glu Gly Asn Pro Gly  
405 410 415

Pro Asp Gly Ala Pro Gly Glu Arg Gly Gly Pro Gly Glu Arg Gly Pro  
420 425 430

Arg Gly Thr Pro Gly Pro Arg Gly Pro Arg Gly Asp Pro Gly Glu Ala  
10 435 440 445

Gly Pro Gln Gly Asp Gln Gly Arg Glu Gly Pro Val Gly Val Pro Gly  
450 455 460

Asp Pro Gly Glu Ala Gly Pro Ile Gly Pro Lys Gly Tyr Arg Gly Asp  
465 470 475 480

15 Glu Gly Pro Pro Gly Ser Glu Gly Ala Arg Gly Ala Pro Gly Pro Ala  
485 490 495

Gly Pro Pro Gly Asp Pro Gly Leu Met Gly Glu Arg Gly Glu Asp Gly  
500 505 510

Pro Ala Gly Asn Gly Thr Glu Gly Phe Pro Gly Phe Pro Gly Tyr Pro  
20 515 520 525

Gly Asn Arg Gly Ala Pro Gly Ile Asn Gly Thr Lys Gly Tyr Pro Gly  
530 535 540

Leu Lys Gly Asp Glu Gly Glu Ala Gly Asp Pro Gly Asp Asp Asn Asn  
545 550 555 560

331/335

Asp Ile Ala Pro Arg Gly Val Lys Gly Ala Lys Gly Tyr Arg Gly Pro  
565 570 575

Glu Gly Pro Gln Gly Pro Pro Gly His Gln Gly Pro Pro Gly Pro Asp  
580 585 590

5 Glu Cys Glu Ile Leu Asp Ile Ile Met Lys Met Cys Ser Cys Cys Glu  
595 600 605

Cys Lys Cys Gly Pro Ile Asp Leu Leu Phe Val Leu Asp Ser Ser Glu  
610 615 620

Ser Ile Gly Leu Gln Asn Phe Glu Ile Ala Lys Asp Phe Val Val Lys  
10 625 630 635 640

Val Ile Asp Arg Leu Ser Arg Asp Glu Leu Val Lys Phe Glu Pro Gly  
645 650 655

Gln Ser Tyr Ala Gly Val Val Gln Tyr Ser His Ser Gln Met Gln Glu  
660 665 670

15 His Val Ser Leu Arg Ser Pro Ser Ile Arg Asn Val Gln Glu Leu Lys  
675 680 685

Glu Ala Ile Lys Ser Leu Gln Trp Met Ala Gly Gly Thr Phe Thr Gly  
690 695 700

Glu Ala Leu Gln Tyr Thr Arg Asp Gln Leu Leu Pro Pro Ser Pro Asn  
20 705 710 715 720

Asn Arg Ile Ala Leu Val Ile Thr Asp Gly Arg Ser Asp Thr Gln Arg  
725 730 735

Asp Thr Thr Pro Leu Asn Val Leu Cys Ser Pro Gly Ile Gln Val Val  
740 745 750

332/335

Ser Val Gly Ile Lys Asp Val Phe Asp Phe Ile Pro Gly Ser Asp Gln  
755 760 765

Leu Asn Val Ile Ser Cys Gln Gly Leu Ala Pro Ser Gln Gly Arg Pro  
770 775 780

5 Gly Leu Ser Leu Val Lys Glu Asn Tyr Ala Glu Leu Leu Glu Asp Ala  
785 790 795 800

Phe Leu Lys Asn Val Thr Ala Gln Ile Cys Ile Asp Lys Lys Cys Pro  
805 810 815

Asp Tyr Thr Cys Pro Ile Thr Phe Ser Ser Pro Ala Asp Ile Thr Ile  
10 820 825 830

Leu Leu Asp Gly Ser Ala Ser Val Gly Ser His Asn Phe Asp Thr Thr  
835 840 845

Lys Arg Phe Ala Lys Arg Leu Ala Glu Arg Phe Leu Thr Ala Gly Arg  
850 855 860

15 Thr Asp Pro Ala His Asp Val Arg Val Ala Val Val Gln Tyr Ser Gly  
865 870 875 880

Thr Gly Gln Gln Arg Pro Glu Arg Ala Ser Leu Gln Phe Leu Gln Asn  
885 890 895

Tyr Thr Ala Leu Ala Ser Ala Val Asp Ala Met Asp Phe Ile Asn Asp  
20 900 905 910

Ala Thr Asp Val Asn Asp Ala Leu Gly Tyr Val Thr Arg Phe Tyr Arg  
915 920 925

Glu Ala Ser Ser Gly Ala Ala Lys Lys Arg Leu Leu Leu Phe Ser Asp  
930 935 940

333/335

Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys Ala Val Gln  
 945                      950                      955                      960  
 Glu Ala Gln Arg Ala Gly Ile Glu Ile Phe Val Val Val Val Gly Arg  
                          965                      970                      975  
 5    Gln Val Asn Glu Pro His Ile Arg Val Leu Val Thr Gly Lys Thr Ala  
                          980                      985                      990  
 Glu Tyr Asp Val Pro Tyr Gly Glu    Ser His Leu Phe Arg    Val Pro Ser  
                          995                      1000                      1005  
 Tyr Gln    Ala Leu Leu Arg Gly    Val Phe His Gln Thr    Val Ser Arg  
 10           1010                      1015                      1020  
 Lys Val    Ala Leu Gly  
                          1025

15    &lt;210&gt;    110

&lt;211&gt;    338

&lt;212&gt;    PRT

&lt;213&gt;    Homo sapiens

&lt;220&gt;

20    &lt;221&gt;    Lumican precursor

&lt;222&gt;    (1)..(338)

&lt;223&gt;    Accession No. as of 29 August 2003: P51884

&lt;400&gt;    110

334/335

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
1 5 10 15  
Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln  
20 25 30  
5 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro  
35 40 45  
Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val  
50 55 60  
Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His  
10 65 70 75 80  
Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile  
85 90 95  
Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe  
100 105 110  
15 Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu  
115 120 125  
Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu  
130 135 140  
Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn  
20 145 150 155 160  
Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val  
165 170 175  
Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser  
180 185 190



335/335

Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu  
195 200 205

Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr  
210 215 220

5 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu  
225 230 235 240

Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu  
245 250 255

Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val  
10 260 265 270

Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys  
275 280 285

Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser  
290 295 300

15 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser  
305 310 315 320

Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr  
325 330 335

Leu Asn